



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 132448

TO: James Schultz
Location: rem/2d18/2c18
Art Unit: 1635
Monday, September 20, 2004

Case Serial Number: 09/227881

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Examiner Schultz,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Toby Port

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STIC-Biotech/ChemLib

132448

mej

From: Schultz, James
Sent: Tuesday, September 14, 2004 11:18 AM
To: STIC-Biotech/ChemLib
Subject: Seq Search 09/227,881

RECEIVED
SEP 14 2004
(STIC)

Hello,
Could you please run a standard nucleotide sequence search on SEQ ID NO: 34 in the above entitled case?

Thanks,
Doug Schultz

James Douglas Schultz, PhD
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(Office) REM 2D18
(Mail) REM 2C18
(571) 272-0763

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search
NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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Mon Sep 20 15:02:12 2004

us-09-227-881-34.rge

Page 1

GenCore version 5.1.6
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model

Run on: September 19, 2004, 12:16:22 (without alignments) 11575.271 Million cell updates/sec

Title: US-09-227-881-34

Perfect score: 5271

Sequence: 1 attctgttcagttaccctc.....tcgggcacgagccagcaagg 5271

Scoring table:

Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: GenEmbl:*

1: gb_ba:*

2: gb_hcg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_to:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_to:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_hcg_hum:*

31: em_hcg_inv:*

32: em_hcg_other:*

33: em_hcg_mus:*

34: em_hcg_pln:*

35: em_hcg_rod:*

36: em_hcg_mam:*

37: em_hcg_vrt:*

38: em_sy:*

39: em_hlgo_hum:*

40: em_hlgo_mus:*

41: em_hlgo_other:*

Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Match	Length	DB	ID	Description
1	5271	100.0	5271	6	BD237961	BD237961 Nucleic a
2	5271	100.0	5271	6	AR242771	AR242771 Sequence
3	5271	100.0	5300	6	AF007562	AF007562 Homo sapi
4	5271	100.0	6169	6	AR123665	AR123665 Sequence
5	5271	100.0	6169	6	BD237936	BD237936 Nucleic a
6	5271	100.0	6169	6	AR242746	AR242746 Sequence
7	5271	100.0	6169	6	BD065041	BD065041 Methods f
8	5246.4	99.5	5299	6	BD065039	BD065039 Methods f
9	5246.4	99.5	5300	6	AR123663	AR123663 Sequence
10	5246.4	99.5	5300	6	BD237934	BD237934 Nucleic a
11	5246.4	99.5	5300	6	AR242744	AR242744 Sequence
12	5232.4	99.3	79376	9	HS45436	298750 Human DNA s
13	5224.4	99.1	5304	6	AR123664	AR123664 Sequence
14	5224.4	99.1	5304	6	BD237935	BD237935 Nucleic a
15	5224.4	99.1	5304	6	AR242745	AR242745 Sequence
16	5224.4	99.1	5304	6	BD065040	BD065040 Methods f
17	5181.4	98.3	170425	2	AC024490	AC024490 Homo sapi
18	1804.4	34.2	2800	6	AR212844	AR212844 Sequence
19	1804.4	34.2	2800	6	BD225246	BD225246 Remedies
20	1804.4	34.2	2800	9	HSMYOC1	AF049791 Homo sapi
21	432.6	8.2	1311	9	AY19012861	AY190128 Macaca fa
22	394.4	7.5	476	6	BD103416	BD103416 Gene rela
23	394.4	7.5	476	6	BD176938	BD176938 Gene rela
24	394.4	7.5	1086	9	HSGICRA1	297171 Homo sapien
25	394.4	7.5	1228	9	AS0068861	AB006886 Homo sapi
26	227	4.3	227	6	BD237965	BD237965 Nucleic a
27	227	4.3	227	6	AR242775	AR242775 Sequence
28	227	4.3	283	6	BD237964	BD237964 Nucleic a
29	227	4.3	283	6	AR242774	AR242774 Sequence
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31	211	4.0	23704	10	AF289236	AF289236 Mus muscu
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35	190.8	3.6	16525	10	AF289235	AF289235 Rattus no
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37	189	3.6	175627	9	AC0107905	AC0107905 Homo sapi
38	189	3.6	198857	9	AC012404	AC012404 Homo sapi
39	187.8	3.6	97037	9	AC004573	AC004573 Homo sapi
40	187.8	3.6	135838	9	HMMXMD703	AC0045973 Homo sapi
41	187.6	3.6	90906	9	AC079767	L78810 Homo sapien
42	187.6	3.6	19367	2	AC009409	AC079767 Homo sapi
43	187.4	3.6	139776	9	AL160165	AC009409 Homo sapi
44	185.8	3.5	1001	11	G73164	AL160165 Human DNA
45	185.8	3.5	76727	9	HS821D11	G73164 GL3-2 Human

ALIGNMENTS

RESULT 1
BD237961
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

BD237961
Nucleic acids, kits, and methods for the diagnosis, prognosis and
treatment of glaucoma and related disorders.
BD237961.1 GI:33047731
JP 2002534135-A/28.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 5271)
Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.
Nucleic acids, kits, and methods for the diagnosis, prognosis and

FEATURES
Source Location/Qualifiers
CC treatment of glaucoma and related disorders
FH Key Location/Qualifiers
FT Source 1..5271
FT 1..5271
Location/Qualifiers
1..5271
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 5271; DB 6; Length 5271;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATCTTGTTCAGTTTCTCTCAGGGCTATTATGAATGAATGAGTATACCAATGGAAG	60
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QY	61	TCTCTAATACCTGTATAGCCTCCATTCGATGTATGCTCTTGGCAGATGAAGATCA	120
DB	61	TCTCTAATACCTGTATAGCCTCCATTCGATGTATGCTCTTGGCAGATGAAGATCA	120
QY	121	GGAGAAGAGATGATCCAGTTAGCCAGTGTCCAGGCTGTGTCTCTTATTTAATGA	180
DB	121	GGAGAAGAGATGATCCAGTTAGCCAGTGTCCAGGCTGTGTCTCTTATTTAATGA	180
QY	181	CAGATGTCTCTCTGACAGAACTTCTTCAGGAAATCATCATCAATATGTAATC	240
DB	181	CAGATGTCTCTCTGACAGAACTTCTTCAGGAAATCATCATCAATATGTAATC	240
QY	241	CATCAACACGAGGCTTAAGAAACAGAAATGAGATGGGCACTTGGCCAGAAAAATG	300
DB	241	CATCAACACGAGGCTTAAGAAACAGAAATGAGATGGGCACTTGGCCAGAAAAATG	300
QY	301	GAGAGCAATATATGATGAAAAATAAATTTCCCTTGTCTTATTTTCAAGAAAAATG	360
DB	301	GAGAGCAATATATGATGAAAAATAAATTTCCCTTGTCTTATTTTCAAGAAAAATG	360
QY	361	ATGAGGACCAATATATGAAATAGAAAAACAGCTCAGAAAAAGATGTTCCAAATTG	420
DB	361	ATGAGGACCAATATATGAAATAGAAAAACAGCTCAGAAAAAGATGTTCCAAATTG	420
QY	421	TAAATTAAGTATTTGTTCTTGGGAGAGACTTCATGATGAGCTTGAATGGAAAAATG	480
DB	421	TAAATTAAGTATTTGTTCTTGGGAGAGACTTCATGATGAGCTTGAATGGAAAAATG	480
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DB	781	GACATGTTTAAAGGCAACAGAAATGTAAGCTTGAAGCTTCAAGAGCAGTGTCCCT	840
QY	841	GGAGCCCTGAGGCTTGTGCTTTAGGAGGCAAGTTTCTTAAGAAATCTTAAGAA	900
DB	841	GGAGCCCTGAGGCTTGTGCTTTAGGAGGCAAGTTTCTTAAGAAATCTTAAGAA	900
QY	901	TTGAAAGATCATGATTTTAAACATTTTAAAGTATTAAGTATTAAGTATTAAG	960
DB	901	TTGAAAGATCATGATTTTAAACATTTTAAAGTATTAAGTATTAAGTATTAAG	960
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DB	1021	GGATAGGTCAGAAATCATTAAGAAATCACTGTGCCATCTTAACCTTTTCAAGAT	1080
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QY	1261	TACAGCCAGAAAGCTCGGTGAGGAGGCTGTGTCTTAACCTGACCTGATGCTTAC	1320
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QY	1321	ACTGAGCTCACTGCAACTCTGCTCCAGGTTCAAGAAATCTGCTGCAAGCTTCC	1380
DB	1321	ACTGAGCTCACTGCAACTCTGCTCCAGGTTCAAGAAATCTGCTGCAAGCTTCC	1380
QY	1381	CGGCTAGCTGAGGCTTAAGGCGCAAGCCCGGCTAATTTTGTATGTATGATGAG	1440
DB	1381	CGGCTAGCTGAGGCTTAAGGCGCAAGCCCGGCTAATTTTGTATGTATGATGAG	1440
QY	1441	GTTTCACCATATTAAGCCGCTGTGTGATCTGATCCTCAGGTGATCCACCACTTC	1500
DB	1441	GTTTCACCATATTAAGCCGCTGTGTGATCTGATCCTCAGGTGATCCACCACTTC	1500
QY	1501	AGCTCTTAAGGCTGAGGCTTAAGGCGCAAGCCCGGCTAATTTTGTATGTATGAG	1560
DB	1501	AGCTCTTAAGGCTGAGGCTTAAGGCGCAAGCCCGGCTAATTTTGTATGTATGAG	1560
QY	1561	TTAATTAAGGATTAAGTATGATTTTAAACCAAGGGAACAGCAAAAGCTGTGA	1620
DB	1561	TTAATTAAGGATTAAGTATGATTTTAAACCAAGGGAACAGCAAAAGCTGTGA	1620
QY	1621	TAAATTAAGGATTTCTGGATGAGGGAATGTGCAATGAGCTGTGCTGATCCAGAC	1680
DB	1621	TAAATTAAGGATTTCTGGATGAGGGAATGTGCAATGAGCTGTGCTGATCCAGAC	1680
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Qy 1921 TGGGTGCTGTAGCAACTGCGACCCGAGCTGCACTGGTTGTTTATCACTCTAG 1980
Db 1921 TGGGTGCTGTAGCAACTGCGACCCGAGCTGCACTGGTTGTTTATCACTCTAG 1980
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Db 3061 GATTTTGAAGAGGAG 3120
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Qy 3541 GTTCTTGAAG 3600
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DB 1321 ACCTGAGCTCACTGACATCTCTGCTCTCCAGGTTCAAGCAATCTCTGCTCAAGCTCTC 1380
QY 1381 CGGATGAGCTGAGCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440
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Db	2701	ATAAAGCAGCTTTAAATTCACAGGCTGATAGGCTTTCCCTTACAAAGGCTTAT	2760
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Db	2761	TTTAAATGGAAATATAGGAAGCCAGCTCATTTCTTAGCCCTTAAATCAAGGAAGAGTAC	2820
Oy	2821	TGAGAGCTTTCTTCATATGCTCTTCGAGCACTACAGCCAGTGAGGACTTGACTTA	2880
Db	2821	TGAGAGCTTTCTTCATATGCTCTTCGAGCACTACAGCCAGTGAGGACTTGACTTA	2880
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Db	2941	GGTTGGCTGAGCAAGCTTGAGCAATGATCTTCCTTCCCTGAGCCATTAATCTTCTGCT	3000
Oy	3001	ATTAAGACCCCTTGACGCTCTGCTGCTTGGAACACTCCCTGCTGATTCCTGTAAGGG	3060
Db	3001	ATTAAGACCCCTTGACGCTCTGCTGCTTGGAACACTCCCTGCTGATTCCTGTAAGGG	3060
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Oy	3301	GGTAGCTTTTGCTTGCAATTCAAAACTGGCCACAGACGATGGAATATGCCAGATG	3360
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Db	3361	TTTAACTTTTCAACCTGACACGACCCACAGCCTCAGATGATCTGTGACACAGG	3420
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Db	3421	AGTAGCTTCACGCGCAAGGAGGAAAGAAAGAAAGAGAGGATATGATGACAGAAAG	3480
Oy	3481	ACAGATTCATCAAGGGCAGTGGGAATGACACAGGATTAATAGTCAACGATACCTGG	3540
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Oy	3661	GTAGTACTGAGGCTGTAAATTAATTTCTCTTATTAAGAACTCTTTTCTCTGT	3720
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D	3721	GGAGTTAGCAGACAAAGGCGCAATCCCGTTTCTTTTAAACGAAAGAAAACATTCCTTAAGG	3780
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D	3781	TAAAGCCAAACGATTCACGCTAGCTGTCTGCTGACTATATGAATGGTTTTTGGAAAAAT	3840
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D	4021	AGTTGGAAATATTTACTCTCAAGATATGACACTGTTGGTATTAACAACATAAAGT	4080
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D	4141	TTATGGCTATTCGCATTGCTTTTGGTTTTCTCTTGGGTTATTAATGTAAAGAG	4200
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D	4321	CTCAAGAGGTATATACAGTACCTGATTTTGGCATTTGCAATGAAATTCACACAT	4380
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D	4441	CTTTGAAATAGACCTGCTGAGATTTGTTTTTAACATTAATAAAACATGTTTAA	4500
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D	4501	ATTTGATATTTTGGATATCATATTTATTAATCATTTGTTCTTGTATCTATATTT	4560
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D	4561	ATAATATTGAAACATCTTTCTGAGAGATTTCCACAGATTCACCAATGAGTCTTGG	4620
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D	4741	AGGAGGGAATCTGCGGCTTCTATAGGAAGCTCTCCCTGAGGCTGGAAGGCTGCTC	4800
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[illegible]

RESULT 3	LOCUS	DEFINITION	VERSION
AF007562	5300 bp	DNA	
AF007562	Homo sapiens trabecular meshwork inducible glucocorticoid response protein (TIGR) gene, promoter region and partial mRNA sequence.	linear	PRI 18-MAR-1998
AF007562			
AF007562.1	GI:2970123		

SOURCE	Human sapiens (human)
ORGANISM	Human sapiens
REFERENCE	Emkaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 530)
AUTHORS	Nayyer, T. D., Chen, P., Huang, W. D., Chen, H., Johnson, D. and Polasky, J. R.
TITLE	Gene structure and properties of TIGR, an olfactomedin-related

JOURNAL. Biol. Chem. 273 (11), 6341-6350 (1998)
MEDLINE 98165818
PUBMED 9497363
2 (bases 1 to 5300)
Nguyen, T.D., Chen, P., Chen, H. and Polansky, J.R.
Direct Submission
Submitted (10-JUN-1997) Ophthalmology, University of California
Francisco, 10 Kihram Street, San Francisco, CA 94143-0730, USA
JOURNAL

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mRNA
5272. .55300

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ORIGIN
/product="tubercular meshwork inducible glucocorticoid
response protein"
/note="additional 3' sequence deposited as TIGR mRNA with
GenBank Accession Number U85257"

Query Match	100.0%;	Score 5271;	DB 9;	Length 5300;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 5271; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

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Db	1	ATCTTGGTCACTTAACTCTCAGGGCTATATGAAATGAAATGAGTAACCAATGTGAAG	60
OY	61	TCCATAAACGTATAGCTCCATTCGGATGATATGCTTTGGCAGGATGATAAAGATCA	120
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OY	121	GGAGAGGAGATATCCAGCTTAGCCAAAGTGTCCAGGCTGTCTGCTCTTATTTAGTGA	180
Db	121	GGAGAGGAGATATCCAGCTTAGCCAAAGTGTCTGCTGCTCTTATTTAGTGA	180
OY	181	CAGATTTGCTCTTACAGAGAGCTATTTCTCAGGAAACATCATCATATGTGTAATC	240
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LOCUS DEFINITION Sequence 3 from patent US 6171788.
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VERSION ARI123665.1 GI:14109026
KEYWORDS
SOURCE Unknown.
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ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 6169)
AUTHORS Nguyen T.D., Polansky, J.R., Chen, P. and Chen, H.
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JOURNAL Patent: US 6171788-A 3 09-JAN-2001;
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 Nucleic acids, kits, and methods for the diagnosis, prognosis and treatment of glaucoma and related disorders.
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 BD237936
 VERSION
 JP 2002534135-A/3.
 KEYWORDS
 JP 2002534135-A/3.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 6169)
 Nguyen,T.D., Polansky,V.R., Chen,P. and Chen,H.
 Nucleic acids, kits, and methods for the diagnosis, prognosis and treatment of glaucoma and related disorders
 Patent: JP 2002534135-A 3 15-OCT-2002;
 THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
 JOURNAL
 OS Homo sapiens (human)
 PN JP 2002534135-A/3
 PD 15-OCT-2002
 PF 11-JAN-2000 JP 2000593777
 PR 11-JAN-1999 US 09/227881,07-MAY-1999 US 09/306828 PI
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 C12N15/09,A61K31/573,A61K45/00,A61P27/06,C12N1/15,C12N1/19, PC
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 PC C12N5/10,C12Q1/68,G01N33/53,G01N33/566,C12N15/00,C12N5/00 CC
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LOCUS AR242746
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ACCESSION AR242746
VERSION AR242746.1 GI:27289385
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 6169)
AUTHORS Nguyen,T.D., Polansky,V.R., Chen,P. and Chen,H.
TITLE Nucleic acids, kits, and methods for the diagnosis, prognosis and
treatment of glioma and related disorders
JOURNAL Patent: US 6475724-A 3 05-NOV-2002;
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Location/Qualifiers
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C12N15/12, C12Q1/68, C07K14/47, A61K31/70
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CC Topology: Linear;
CC Methods for the diagnosis, prognosis and
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ORIGIN

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DB 61 TCCATTAACCTGTATGCGCTCCATTCGAGATGATGCTTGGCAGAGATTAAGATCA 120

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Db	4741	AGGGGGGAATTCGCGCTTGTATAGAAATGCTCTCCCTGGAAGCTGGTAGGGTCTGTC	4800
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Db	4801	CTTGATTTGCTRGCGCTGTATTTTCTGTGCCCGGCTAAGTCTCTAAAGGACATGTTT	4860
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Db	5161	CCGTGTGACAGCCCCACCCAGCCGTACAGTGGCCACCCCTGTCTCTTCCCATTAAGGGCTG	5220		
QY	5221	GCTCCCCAGATATATAAACCTCTCTGTAGAGTCGGGAGCATGAGCCAGCAAG	5211		
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DEFINITION	BD065039	Methods for the diagnosis, prognosis and treatment of glaucoma and related disorders.			
ACCESSION	BD065039				
VERSION	BD065039.1	GI:22610642			
KEYWORDS	JP 2001509669-A/1.				
SOURCE	unidentified				
ORGANISM	unclassified				
REFERENCE	1 (bases 1 to 5299)				
AUTHORS	Nguyen,T.D., Polanski,J.R., Chen,P. and Chen,H.				
TITLE	Methods for the diagnosis, prognosis and treatment of glaucoma and related disorders				
JOURNAL	Patent: JP 2001509669-A 1 24-JUN-2001;				
COMMENT	THE REGENTS OF THE UNIVERSITY OF CALIFORNIA				
	OS Unidentified				
	PN JP 2001509669-A/1				
	PD 24-JUN-2001				
	PT 28-JAN-1998 JP 1998532017				
	FR 08-JAN-1997 US 08/791154,26-SEP-1997 US				08/938669 PT
	THAI D NGUYEN,JON R POLANSKY,PU CHEN,HUA CHEN PC				
	C12N15/12,C12Q1/68,C07K14/47,A61K31/70				
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	CC Topology: Linear;				
	CC Methods for the diagnosis, prognosis and treatment of glaucoma				
	CC and related				
	CC disorders				
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ORIGIN					
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Best Local Similarity	99.9%;	Pred. No. 0;			
Matches 5269;	Conservative 0;	Mismatches 1;	Indels 2;	Gaps 2;	
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Db	61	TCTTATAACTGTATAGCTTCATTTGGAGATGTGCTTTGGCAGAGATGATTAAGATCA	120		
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 PC C12N5/10, C1201/68, G01N3/53, G01N3/566, C12N15/00, C12N5/00 CC
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 and
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Query Match 99.5%; Score 5246.4; DB 6; Length 5300;
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Query Match	Best Local Similarity	Score	Pred. No. of	Mismatches	Indels	Gaps
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ACCESSION	AR242744					
VERSION	AR242744.1	GI:27289383				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 5300)					
TITLE	Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.					
JOURNAL	Nucleic acids, kits, and methods for the diagnosis, prognosis and treatment of glaucoma and related disorders					
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VERSION	AR242744.1	GI:27289383				
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ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 5300)					
TITLE	Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.					
JOURNAL	Nucleic acids, kits, and methods for the diagnosis, prognosis and treatment of glaucoma and related disorders					
FEATURES	Patent: US 6475724-A 1 05-NOV-2002;					
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[illegible]

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Human DNA sequence from clone RPJ-454G6 on chromosome 1q24, complete sequence.			

ACCEPTED 298750
 VERSION 298750.1 GI:2687277
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 75376)
 Pavltz/R.
 REFERENCE Direct Submission
 TITLE Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
 JOURNAL

COMMENT

Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
On Feb 14, 1998 this sequence version replaced gi:2465060.

Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquerry@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate strand. Regions that were not sequenced were indicated by a dash (-). Chemistry or coverage by high quality data (i.e., phred quality ≥ 30) or an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em1, EMBL; Sw1, SWISSPROT; Tr1, TREMBL; Wg1, WORMPEP; Information on the WORMPEP database can be found at <http://www.wormbase.org>.

was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/projects/c_elegans/wormmap this sequence

<http://www.sanger.ac.uk/H33/Ch11.RP3-155466> is from the library RP3-3 constructed by the group of [pieter.dejong](mailto:pieter.dejong@chori.org). For further details see <http://www.chori.org/baepac/home.htm>

VECTOR: pCYPAC2

IMPORTANT: This sequence is not the entire insert of clone RP3-155466. It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RP3-45608 is at 1 in this sequence. The true left end of clone RP4-56089 is at 79273 in this sequence.

FEATURES
source

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CDS

Query Match	99.3%;	Score 5232.4;	DB 9;	Length 79376;
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Qy 1861 TGAAGCCCCGGCAGAGGTTTCTCTCCAGCTGGGAGGAGCCCTCAGCAACCCGGGCTC 1920
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Qy 1921 TGGGTCCTGAGCAACCTGCAAGCCGCTGCACTGATGTTTGTATATCACTCTACG 1980
Db TGGGTCCTGAGCAACCTGCAAGCCGCTGCACTGATGTTTGTATATCACTCTACG 66486
Qy 1981 GACCTGTGCTTTTATTTCTGTGTGACTGTCATTCATTCAGGCAATTCATTAACAT 2040
Db GACCTGTGCTTTTATTTCTGTGTGACTGTCATTCATTCAGGCAATTCATTAACAT 66426
Qy 2041 TATTAGATCTTAATCTGCGACACACAGACAAATGCTGACAAAGCACTGCT 2100
Db TATTAGATCTTAATCTGCGACACACAGACAAATGCTGACAAAGCACTGCT 66366
Qy 2101 CCTACCTCGTGAAGTGAACAGTTCTCATGGAAGAAGTCAAGAAATTAATAGCC 2160
Db CCTACCTCGTGAAGTGAACAGTTCTCATGGAAGAAGTCAAGAAATTAATAGCC 66306
Qy 2161 GCCAATTAACCCAGTGTGAAGAAAGAAATTAACACCATCTTGAAGATTTGCGC 2220
Db GCCAATTAACCCAGTGTGAAGAAAGAAATTAACACCATCTTGAAGATTTGCGC 66246
Qy 2221 AGCATCCCTTAACAGGCACTCCCTAGAGCCCGCTGCTGCTCATCAAGCTGCACTGAG 2280
Db AGCATCCCTTAACAGGCACTCCCTAGAGCCCGCTGCTGCTCATCAAGCTGCACTGAG 66186
Qy 2281 CCCCAGCCGAGTCTTCAAGCTCTCTCATCAAGCTGCACTGAGCTGAGCT 2340
Db CCCCAGCCGAGTCTTCAAGCTCTCTCATCAAGCTGCACTGAGCTGAGCT 66126
Qy 2341 GCTGCTCCCGGAAATGCTCCGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 2400
Db GCTGCTCCCGGAAATGCTCCGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 66066
Qy 2401 CAGAAAGAAATGAGAGGAAATAGTCTAAAGAGATCTGAGAGGAGCAGTGTTC 2460
Db CAGAAAGAAATGAGAGGAAATAGTCTAAAGAGATCTGAGAGGAGCAGTGTTC 66006
Qy 2461 CTCAGAGGAAAGGGCTCTCAAGTCCAGAGAAATTCAGAGGTGGGACTGCAAGGAG 2520
Db CTCAGAGGAAAGGGCTCTCAAGTCCAGAGAAATTCAGAGGTGGGACTGCAAGGAG 65946
Qy 2521 TGGGAGCTGTGGGCTGAGGAGGTGTGTAAGGCAAGAAATGGAAGGCAAGCTGA 2580
Db TGGGAGCTGTGGGCTGAGGAGGTGTGTAAGGCAAGAAATGGAAGGCAAGCTGA 65887

Db 65886 TGGGAGCGCTGGGGCTGAGCGGGTCTGAAAGCGAGAGGTGAAAGGCGAAAGGCTGAA 65827
Qy 2581 GCTGCCAGATGTTCAAGTGTGTTTCAAGGCGGCTGGAGATTTCCGTTGCTTCTGTGAG 2640
Db 65826 GCTGCCAGATGTTCAAGTGTGTTTCAAGGCGGCTGGAGATTTCCGTTGCTTCTGTGAG 65767
Qy 2641 CTTTATCTTTCTCTGCTTGGAGAGAGAAAGCTATTTCATGAGAGGATGCAATTTC 2700
Db 65766 CTTTATCTTTCTCTGCTTGGAGAGAGAAAGCTATTTCATGAGAGGATGCAATTTC 65707
Qy 2701 ATAAAGTCAGCTGTAAATTCAGAGGTGTGACATGAGTTTCTTCCAGAGGCTTTAT 2760
Db 65706 ATAAAGTCAGCTGTAAATTCAGAGGTGTGACATGAGTTTCTTCCAGAGGCTTTAT 65647
Qy 2761 TTAATGGAAATTAAGAGAGCGAGCTCATTTCCCTAGGCGCTTAATTCAGAGAGATGAC 2820
Db 65646 TTAATGGAAATTAAGAGAGCGAGCTCATTTCCCTAGGCGCTTAATTCAGAGAGATGAC 65587
Qy 2821 TGAAGTCTTTCTTCAATGCTTCTTGGGCACTAATCAAGCCCTGTGTGACCTTGA 2880
Db 65586 TGAAGTCTTTCTTCAATGCTTCTTGGGCACTAATCAAGCCCTGTGTGACCTTGA 65527
Qy 2881 TCGAAGAGCGTGAAGAACTTGGAAATGAGAGAGTGGTTTCTTCTGTTCTGCAAT 2940
Db 65526 TCGAAGAGCGTGAAGAACTTGGAAATGAGAGAGTGGTTTCTTCTGTTCTGCAAT 65467
Qy 2941 GGTGGCTGTGCAAGCGTGGGCAAGTGTCTCTCTCTGCGGCAATGCTTCTGTCT 3000
Db 65466 GGTGGCTGTGCAAGCGTGGGCAAGTGTCTCTCTCTGCGGCAATGCTTCTGTCT 65407
Qy 3001 ATAAAGACCTTGGAGCTCTGCTTCTGTAAGTCCCTGATGATCTTCTGTGAGG 3060
Db 65406 ATAAAGACCTTGGAGCTCTGCTTCTGTAAGTCCCTGATGATCTTCTGTGAGG 65347
Qy 3061 GGATGTGAGAGGAGAGAGAGAGAGAGAGTGGAGAGCTGAGAGAGAGAGAGAGG 3120
Db 65346 GGATGTGAGG 65287
Qy 3121 GGAAG 3180
Db 65286 GGAAG 65227
Qy 3181 CAGGACCGAG 3240
Db 65226 CAGGACCGAG 65167
Qy 3241 TCCCTAAGCATGAG 3300
Db 65166 TCCCTAAGCATGAG 65107
Qy 3301 GGTAGCTTTTGGCTTGGCAATCAAAAAGTGGGCGAGAGAGAGAGAGAGAG 3360
Db 65106 GGTAGCTTTTGGCTTGGCAATCAAAAAGTGGGCGAGAGAGAGAGAGAGAG 65047
Qy 3361 TTAAGCTTTTCAAGCTTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420
Db 65046 TTAAGCTTTTCAAGCTTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 64987
Qy 3421 AGTGAAGTGAAG 3480
Db 64986 AGTGAAGTGAAG 64927
Qy 3481 AAGAGATGATCAAG 3540
Db 64926 AAGAGATGATCAAG 64867
Qy 3541 GTTCTAG 3600
Db 64866 GTTCTAG 64807
Qy 3601 CCGATTTCTTAATATATTTTCTTCAAGCTGAGAGAGAGAGAGAGAGAGAG 3660

Db 64806 CCGATTTCTTAATATATTTTCTTCAAGCTGAGAGAGAGAGAGAGAGAGAG 64747
Qy 3661 GTAGTAACTGAGAGCTGTAAGAGATTAATTAATTAATTAATTAATTAATTAATTA 3720
Db 64746 GTAGTAACTGAGAGCTGTAAGAGATTAATTAATTAATTAATTAATTAATTAATTA 64687
Qy 3721 GGAAGTGAAG 3780
Db 64686 GGAAGTGAAG 64627
Qy 3781 TAAAGCCAAACAGATTCAGAGCTGAGCTTGTGCTAATTAATTAATTAATTAAT 3840
Db 64626 TAAAGCCAAACAGATTCAGAGCTGAGCTTGTGCTAATTAATTAATTAATTA 64567
Qy 3841 CATTCAGAGAGAGTGAATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3900
Db 64566 CATTCAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 64507
Qy 3901 TAAACAAACAGAGCTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3959
Db 64506 TAAACAAACAGAGCTGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 64447
Qy 3959 AAGATTAAGATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4019
Db 64446 AAGATTAAGATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 64388
Qy 4020 CAGTTTGAAGATTTTACTTCAAGATTAATTAATTAATTAATTAATTAATTAATTA 4079
Db 64387 CAGTTTGAAGATTTTACTTCAAGATTAATTAATTAATTAATTAATTAATTAATTA 64328
Qy 4080 TTGCTCAAGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4139
Db 64327 TTGCTCAAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 64268
Qy 4140 TTTATGGATATGCAATTTGCTTTTGTGTTTCTCTTGGTTATTAATTAATTA 4199
Db 64267 TTTATGGATATGCAATTTGCTTTTGTGTTTCTCTTGGTTATTAATTAATTA 64208
Qy 4200 GGAATTAATTAAG 4259
Db 64207 GGAATTAATTAAG 64148
Qy 4260 TTGTTTTCACAGCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4319
Db 64147 TTGTTTTCACAGCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 64088
Qy 4320 ACTCAAG 4379
Db 64087 ACTCAAG 64028
Qy 4380 TTTATCTAATTAAG 4439
Db 64027 TTTATCTAATTAAG 63968
Qy 4440 ACTTGAATTAAG 4499
Db 63967 ACTTGAATTAAG 63908
Qy 4500 AATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4559
Db 63907 AATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 63848
Qy 4560 TATATTTGAAG 4619
Db 63847 TATATTTGAAG 63788
Qy 4620 GCATGACACACAG 4679
Db 63787 GCATGACACACAG 63728
Qy 4680 ATGCAAG 4739
Db 63727 ATGCAAG 63668

[illegible]

Dp	121	GGAAAGAGAGATACACGTTAGCCAAAGTTCAGAGCTTCGTCTTATTTTACTGA	180
Qy	181	CAGATGTTGCTCCTGACAGAGCTATTTCTTCAGAAATCATCATTCATATGCTAATTC	240
Dp	181	CAGATGTTGCTCCTGACAGAGCTATTTCTTCAGAAATCATCATTCATATGCTAATTC	240
Qy	241	CATCAAAACAGAGACTTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGSAAATCCAG	300
Dp	241	CATCAAAACAGAGACTTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGSAAATCCAG	300
Qy	301	GAGAGCAAAATATGATGAAAAATAAACTTTTCCCTTGTGTTTTTAATTCAGAAAAATG	360
Dp	301	GAGAGCAAAATATGATGAAAAATAAACTTTTCCCTTGTGTTTTTAATTCAGAAAAATG	360
Qy	361	ATGAGGACCAAAATCAATGAATAAAGAAAACAGCTCAGAAAAAAGATTTCCAAATTGG	420
Dp	361	ATGAGGACCAAAATCAATGAATAAAGAAAACAGCTCAGAAAAAAGATTTCCAAATTGG	420
Qy	421	TAAATTAAGTATTTGTTCTTGGGAAGACCTCCATGTGAGCTTGATGGSAAATGGAA	480
Dp	421	TAAATTAAGTATTTGTTCTTGGGAAGAACCTCCATGTGAGCTTGATGGSAAATGGAA	480
Qy	481	AAACGTCAAAAGCATATCTGATCAATCCCAAGATGATTAATTTAAAAACCAT	540
Dp	481	AAACGTCAAAAGCATATCTGATCAATCCCAAGATGATTAATTTAAAAACCAT	540
Qy	541	GGCATCACTCGGGGAGGCAAGTTAGSAAAGTCATGTTGCAAAAGACATACATAAC	600
Dp	541	GGCATCACTCGGGGAGGCAAGTTAGSAAAGTCATGTTGCAAAAGACATACATAAC	600
Qy	601	AGCAAAATCAAAATTTCCGCAAAATGCGAGAGSAAATGGGACTGGGAAAGCTTCAATAAC	660
Dp	601	AGCAAAATCAAAATTTCCGCAAAATGCGAGAGSAAATGGGACTGGGAAAGCTTCAATAAC	660
Qy	661	AGTGAATTAGAGAGTTGACATGTTGCGAACAACCTCCCGCTCTATACAGSAAACCAAA	720
Dp	661	AGTGAATTAGAGAGTTGACATGTTGCGAACAACCTCCCGCTCTATACAGSAAACCAAA	720
Qy	721	ATTGACTGCGCTAGACCTGGACTTTCAAGGGAATATGAAAACTAGAGCAAAACAAA	780
Dp	721	ATTGACTGCGCTAGACCTGGACTTTCAAGGGAATATGAAAACTAGAGCAAAACAAA	780
Qy	781	GAAATGCTTAAAGGCAACCAAGACATTTGAGAGCTTCAAAAGACAGATGCCCTCAGCA	840
Dp	781	GAAATGCTTAAAGGCAACCAAGACATTTGAGAGCTTCAAAAGACAGATGCCCTCAGCA	840
Qy	841	GGGACCTGAGCATTTCCTTTAGSAAAGCCAGTTTCTTAAGSAACTTAAAGAACTC	900
Dp	841	GGGACCTGAGCATTTCCTTTAGSAAAGCCAGTTTCTTAAGSAACTTAAAGAACTC	900
Qy	901	TTGAAAGATCATGAATTTTAAACAATTTTAAGTAAACCAATATGCGATGCATATCAG	960
Dp	901	TTGAAAGATCATGAATTTTAAACAATTTTAAGTAAACCAATATGCGATGCATATCAG	960
Qy	961	TTTAGACATGGGTCCCAATTTTAATAAGTCAGGACATCAAGATTAACGATGCCAGCTTC	1020
Dp	961	TTTAGACATGGGTCCCAATTTTAATAAGTCAGGACATCAAGATTAACGATGCCAGCTTC	1020
Qy	1021	GGATAGGTCAGAAATCATATGAATCACTGTGCCCATCTTAACCTTTTCAGATGATC	1080
Dp	1021	GGATAGGTCAGAAATCATATGAATCACTGTGCCCATCTTAACCTTTTCAGATGATC	1080
Qy	1081	TGTCAATAGCCCTCACAACAGGCCGATGTGTGACCTACACAACACATCTACAACTCA	1140
Dp	1081	TGTCAATAGCCCTCACAACAGGCCGATGTGTGACCTACACAACACATCTACAACTCA	1140
Qy	1141	GTCCTCAACCATTTGTTAAGCTGTCATCTAGTAGGCTCCATTACAAATGCACTGCC	1200
Dp	1141	GTCCTCAACCATTTGTTAAGCTGTCATCTAGTAGGCTCCATTACAAATGCACTGCC	1200
Qy	1201	TGTGAGAGCCCATCCCGCTCCACAGSAAAGTCTCCCACTCTATACCTTCGATCAACGATG	1260
Dp	1201	TGTGAGAGCCCATCCCGCTCCACAGSAAAGTCTCCCACTCTATACCTTCGATCAACGATG	1260

QY 1261 TACAGCCAGAGGCTCCGTAGAGGCTGAGGGCTGTGCTTACACCTACCTGATGCTAC 1320
DB 1261 TACAGCCAGAGGCTCCGTAGAGGCTGAGGGCTGTGCTTACACCTACCTGATGCTAC 1320
QY 1321 ACCTGAGCTCACTGCAACCTCTGCTCCAGGTTCAAGCAATTCCTGTCAAGCTCC 1380
DB 1321 ACCTGAGCTCACTGCAACCTCTGCTCCAGGTTCAAGCAATTCCTGTCAAGCTCC 1380
QY 1381 CGGTAGCTGGAGCTACAGGCGGACCCCGCTAATTTTGTATTTGTATGTAAGATGG 1440
DB 1381 CGGTAGCTGGAGCTACAGGCGGACCCCGCTAATTTTGTATTTGTATGTAAGATGG 1440
QY 1441 GTTTCACCATATAGAGCCGCTGTCTTGAACCTCTGACCTCAGGTTATCCACCACTC 1500
DB 1441 GTTTCACCATATAGAGCCGCTGTCTTGAACCTCTGACCTCAGGTTATCCACCACTC 1500
QY 1501 AGCCTCTAAAGTGTGGATTAACAGGCAATGATCAAGGCTCCGCTCAAGGTTAGT 1560
DB 1501 AGCCTCTAAAGTGTGGATTAACAGGCAATGATCAAGGCTCCGCTCAAGGTTAGT 1560
QY 1561 TTAAATAGGATATAGTGAATGCTTAACTAAACCAAGGAAACAGACAAAGGTTGA 1620
DB 1561 TTAAATAGGATATAGTGAATGCTTAACTAAACCAAGGAAACAGACAAAGGTTGA 1620
QY 1621 TAAATTCAGGATTTCTGGATGAGGAAATGCTCCATGAGCTGCTGCTTCCAGAC 1680
DB 1621 TAAATTCAGGATTTCTGGATGAGGAAATGCTCCATGAGCTGCTGCTTCCAGAC 1680
QY 1681 CACTGCTCTCATACCTTTCTCCCTCATCTCTCATTTTCAAGGTAAGTACATTTAT 1740
DB 1681 CACTGCTCTCATACCTTTCTCCCTCATCTCTCATTTTCAAGGTAAGTACATTTAT 1740
QY 1741 CACCATGCTTTTGTGTAAGCTCTCAACATGCTTACGAAATTAAGATTAACATTA 1800
DB 1741 CACCATGCTTTTGTGTAAGCTCTCAACATGCTTACGAAATTAAGATTAACATTA 1800
QY 1801 TTCCATTGGGGCCATCTGTGTGTGTATAGGGGAGAGGGCATACCCCAAGACTCT 1860
DB 1801 TTCCATTGGGGCCATCTGTGTGTGTATAGGGGAGAGGGCATACCCCAAGACTCT 1860
QY 1861 TGAAGCCCCCGGAGAGGTTTCTCTCAAGCTGGGGAGCCCTGCAAGACCCGGGCTC 1920
DB 1861 TGAAGCCCCCGGAGAGGTTTCTCTCAAGCTGGGGAGCCCTGCAAGACCCGGGCTC 1920
QY 1921 TGGGTGTCTGAGCAACCTGCAAGCCGCTGCACTGGTGTGTTTATCACTCTAGG 1980
DB 1921 TGGGTGTCTGAGCAACCTGCAAGCCGCTGCACTGGTGTGTTTATCACTCTAGG 1980
QY 1981 GACCTGTGCTTTTATTTCTGTGTGTACTGTTTATTCATCCAGGATTCATTTGACA 2040
DB 1981 GACCTGTGCTTTTATTTCTGTGTGTACTGTTTATTCATCCAGGATTCATTTGACA 2040
QY 2041 TATGAGTACTTATATCTGCAAGACCAAGACAAATGTGAGCAAGGCTGCTGCTG 2100
DB 2041 TATGAGTACTTATATCTGCAAGACCAAGACAAATGTGAGCAAGGCTGCTGCTG 2100
QY 2101 CTTACTCTGTGAGGTAAGCTTTCTCATGGAAGAGTGCAGAAAGAAATTAATGCA 2160
DB 2101 CTTACTCTGTGAGGTAAGCTTTCTCATGGAAGAGTGCAGAAAGAAATTAATGCA 2160
QY 2161 GCGAATTAAGCCAGGCTGAAGAAAGAAATTAACACATCTTGAAGATTTGGCC 2220
DB 2161 GCGAATTAAGCCAGGCTGAAGAAAGAAATTAACACATCTTGAAGATTTGGCC 2220
QY 2221 AGCATCCCTTAACAAAGGCACTCCCTAGGCCCCCTGCTGCTCCATCTGCCCCGA 2280
DB 2221 AGCATCCCTTAACAAAGGCACTCCCTAGGCCCCCTGCTGCTCCATCTGCCCCGA 2280
QY 2281 CCCCCAAGCCGAGCTTCCAGGCTCCTCTCATAGTCAACGAGCTGCACTGGCT 2340
DB 2281 CCCCCAAGCCGAGCTTCCAGGCTCCTCTCATAGTCAACGAGCTGCACTGGCT 2340
QY 2341 GCCTGCTTCCCGTAAATGCTCTGTGATCTGAGTCACTGAGACTCTTGTGCTCAGGCT 2400
DB 2341 GCCTGCTTCCCGTAAATGCTCTGTGATCTGAGTCACTGAGACTCTTGTGCTCAGGCT 2400
QY 2401 CCAGAAAGAAATGAGAGAGGAACTAGCTTAAACGGAATCTGAGAGGAGCAGGTTTC 2460
DB 2401 CCAGAAAGAAATGAGAGAGGAACTAGCTTAAACGGAATCTGAGAGGAGCAGGTTTC 2460
QY 2461 CTCAGAGGAAAGGGGCTCCACGTCCAGAGAAATTCAGAGAGGTGAGGAGCTGCA 2520
DB 2461 CTCAGAGGAAAGGGGCTCCACGTCCAGAGAAATTCAGAGAGGTGAGGAGCTGCA 2520
QY 2521 TGGGAGCGTGGGCTGAGCGGCTGTGAAAGGCAAGGTAAGGAGGCAAGGCTGAA 2580
DB 2521 TGGGAGCGTGGGCTGAGCGGCTGTGAAAGGCAAGGTAAGGAGGCAAGGCTGAA 2580
QY 2581 GCTGCCAGATGTTGATGTTGATTCACGAGGCTGGAGATTTCCGTTGCTGTGAGC 2640
DB 2581 GCTGCCAGATGTTGATGTTGATTCACGAGGCTGGAGATTTCCGTTGCTGTGAGC 2640
QY 2641 CTTTATCTTTCTCTGCTTGAAGAGAAATTTATTCATGAAAGGATGCAATTC 2700
DB 2641 CTTTATCTTTCTCTGCTTGAAGAGAAATTTATTCATGAAAGGATGCAATTC 2700
QY 2701 ATAAAGTCAAGCTTTAAATTCAGAGGCTGCAAGGTTTCTTCAAGAGGCTTTAT 2760
DB 2701 ATAAAGTCAAGCTTTAAATTCAGAGGCTGCAAGGTTTCTTCAAGAGGCTTTAT 2760
QY 2761 TTAAATGGAATATAGGAACGAGCTCAATTCCTAGGCGGTAAATCAGGAAGAGTAC 2820
DB 2761 TTAAATGGAATATAGGAACGAGCTCAATTCCTAGGCGGTAAATCAGGAAGAGTAC 2820
QY 2821 TGAAGTCTTTTCTTCTTATGTTCTTGGGCACTACTCAAGCTGTGTGAGTGGCTTA 2880
DB 2821 TGAAGTCTTTTCTTCTTATGTTCTTGGGCACTACTCAAGCTGTGTGAGTGGCTTA 2880
QY 2881 TGAAGAGGCTGCAAAACCTTGGAATCAGAGACTGAGTTTCTTCTGTTCTGCAAT 2940
DB 2881 TGAAGAGGCTGCAAAACCTTGGAATCAGAGACTGAGTTTCTTCTGTTCTGCAAT 2940
QY 2941 GGTGCTGTGCAAGCTGGGCAAGTGTCTTCTTCTTCTGAGGCAATGCTCTGCT 3000
DB 2941 GGTGCTGTGCAAGCTGGGCAAGTGTCTTCTTCTTCTGAGGCAATGCTCTGCT 3000
QY 3001 ATAAAGCCTTCAAGCTCTGCTGTTCTGTAACAATTCCTGTAATCTCTGAGGG 3060
DB 3001 ATAAAGCCTTCAAGCTCTGCTGTTCTGTAACAATTCCTGTAATCTCTGAGGG 3060
QY 3061 GATGTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3120
DB 3061 GATGTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3120
QY 3121 GAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3180
DB 3121 GAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3180
QY 3181 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3240
DB 3181 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3240
QY 3241 TCCCTAAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCA 3300
DB 3241 TCCCTAAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCA 3300
QY 3301 GGTAGCTTTTGGCTGAGCTTCAAAAAGTGGGAGGAGGAGGAGGAGGAGGAGG 3360
DB 3301 GGTAGCTTTTGGCTGAGCTTCAAAAAGTGGGAGGAGGAGGAGGAGGAGGAGG 3360
QY 3361 TTAAATCTTACCTGAGCAGCAACCCAGCAGCTCAGAGTGAATGCTGAGAGAGG 3420
DB 3361 TTAAATCTTACCTGAGCAGCAACCCAGCAGCTCAGAGTGAATGCTGAGAGAGG 3420
QY 3421 AGTACCTGAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3480
DB 3421 AGTACCTGAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3480

[illegible]

QY	781	GATGATGTTAAAGGCAACGAAACATGTGAAGCTTCAAGAGCAGAGTGGCCCTCAGCA	84
Db	781	GATGATGTTAAAGGCAACGAAACATGTGAAGCTTCAAGAGCAGAGTGGCCCTCAGCA	840
QY	841	GAGACCTTAGGCATTTGGCTTTAGGAAGCCAGTTTCTTAAAGAACTTAAAGAACTC	900
Db	841	GAGACCTTAGGCATTTGGCTTTAGGAAGCCAGTTTCTTAAAGAACTTAAAGAACTC	900
QY	901	TTGAAAGATCATGAATTTTAACTTTTAACTTAAACAAATGTGGATGACATATACG	960
Db	901	TTGAAAGATCATGAATTTTAACTTTTAACTTAAACAAATGTGGATGACATATACG	960
QY	961	TTTAAACATGGGTCCTCAATTTATTAAGTCAAGGACATCAAGATATACGATGCCAGTCC	102
Db	961	TTTAAACATGGGTCCTCAATTTATTAAGTCAAGGACATCAAGATATACGATGCCAGTCC	102
QY	1021	GGATAGGTCAGAAATCATTAAGAAATCACTGTGTGCCATCTTAATCTTTTACAAATGATC	108
Db	1021	GGATAGGTCAGAAATCATTAAGAAATCACTGTGTGCCATCTTAATCTTTTACAAATGATC	108
QY	1081	TGTCAATAGCCCTACACACAGGCCGAGTGTGCACTCAACACACATCTAACACCCAA	114
Db	1081	TGTCAATAGCCCTACACACAGGCCGAGTGTGCACTCAACACACATCTAACACCCAA	114
QY	1141	GTCGCTCAACCATTTGTAAAGTGTGATCATCTCAAGTAGAGTCCCATTAACAAATGCCACTTCCC	120
Db	1141	GTCGCTCAACCATTTGTAAAGTGTGATCATCTCAAGTAGAGTCCCATTAACAAATGCCACTTCCC	120
QY	1201	TGTGACAGCCCATCTCCGCTCCACAGAGATCTCCCACTCTGACCTTCGATCAAGATGT	126
Db	1201	TGTGACAGCCCATCTCCGCTCCACAGAGATCTCCCACTCTGACCTTCGATCAAGATGT	126
QY	1261	TACAGCAGAAAGCTCCGTGAGAGGTAGAGGTCTGTCTTTAAACCTTACCTGATCTCTAC	132
Db	1261	TACAGCAGAAAGCTCCGTGAGAGGTAGAGGTCTGTCTTTAAACCTTACCTGATCTCTAC	132
QY	1321	ACCTGAGCTCATGCAACCTCTGCTCCACAGGTTCAAGCAATCTCTCTGTCTCAGCTCC	138
Db	1321	ACCTGAGCTCATGCAACCTCTGCTCCACAGGTTCAAGCAATCTCTCTGTCTCAGCTCC	138
QY	1381	CGCGTACTCTGGACCTACAGGCGAGCGCCGCGTAATTTTGTATGTATGATAGAGATGAG	144
Db	1381	CGCGTACTCTGGACCTACAGGCGAGCGCCGCGTAATTTTGTATGTATGATAGAGATGAG	144
QY	1441	GTTTCACCATATTAGCCCGGCTGTGTTGAATCTCTGACTCAAGGTATCCACCACTTC	150
Db	1441	GTTTCACCATATTAGCCCGGCTGTGTTGAATCTCTGACTCAAGGTATCCACCACTTC	150
QY	1501	AGCTCTCTAAAGTCTGGGATTACAGGATGATGATACCGCGCCGCGCAAGGATCAGGT	156
Db	1501	AGCTCTCTAAAGTCTGGGATTACAGGATGATGATACCGCGCCGCGCAAGGATCAGGT	156
QY	1561	TTAATTAAGGAATTAATCTGATGATGTTTACAAACCAACAGGAAACAGCAAAAGCTGGA	162
Db	1561	TTAATTAAGGAATTAATCTGATGATGTTTACAAACCAACAGGAAACAGCAAAAGCTGGA	162
QY	1621	TAAATTCAGGATCTTGGGATGGGAAATGGTGCATGAGCTGCTGCTGATCCCAAC	168
Db	1621	TAAATTCAGGATCTTGGGATGGGAAATGGTGCATGAGCTGCTGCTGATCCCAAC	168
QY	1681	CACAGTGTCTATCACTTTCTCCCTCATCTCAATTTTCAAGGCTAAGTTACATTTTAT	174
Db	1681	CACAGTGTCTATCACTTTCTCCCTCATCTCAATTTTCAAGGCTAAGTTACATTTTAT	174
QY	1741	CACCATGCTTTTGTGTAAAGCTTCCACATGCTTACGAAATTAAGATATACATACTAG	180
Db	1741	CACCATGCTTTTGTGTAAAGCTTCCACATGCTTACGAAATTAAGATATACATACTAG	180
QY	1801	TTCCATTTGGGGCCATCTGTGTGTATATAGGGAGAGAGGCATATCCCAAGAGCTCT	186
Db	1801	TTCCATTTGGGGCCATCTGTGTGTATATAGGGAGAGAGGCATATCCCAAGAGCTCT	186

QY 1861 TGAAGCCCGGAGAGGTTTCCCTCAAGCTGGGGAGCCCTGCAAGCAACCCGGGGTCC 1920
Db 1861 TGAAGCCCGGAGAGGTTTCCCTCAAGCTGGGGAGCCCTGCAAGCAACCCGGGGTCC 1920
QY 1921 TGGGTGCTCGAGGAACCTGCGACGCCCGTCCACTGCTGTTTGTGTTATCACTCTAGG 1980
Db 1921 TGGGTGCTCGAGGAACCTGCGACGCCCGTCCACTGCTGTTTGTGTTATCACTCTAGG 1980
QY 1981 GACCTGTGCTTCTATTTCTGTGTGACTGTTCAATTCAGGCAATTCATGCAATT 2040
Db 1981 GACCTGTGCTTCTATTTCTGTGTGACTGTTCAATTCAGGCAATTCATGCAATT 2040
QY 2041 TATTGACTTCTATATCTGCGAACAACAGCAAAATGTTGAGCAAGCAAGTCACTGC 2100
Db 2041 TATTGACTTCTATATCTGCGAACAACAGCAAAATGTTGAGCAAGCAAGTCACTGC 2100
QY 2101 CCTACCTTGGTGAAGGAGTTCATCTGAGAAAGCGTGAAGAAATTAATAGCA 2160
Db 2101 CCTACCTTGGTGAAGGAGTTCATCTGAGAAAGCGTGAAGAAATTAATAGCA 2160
QY 2161 GCCAACTTAAACCCAGTGTGAAAGAAAGAAATTAACACCACTTGAAGATTGTGCGC 2220
Db 2161 GCCAACTTAAACCCAGTGTGAAAGAAAGAAATTAACACCACTTGAAGATTGTGCGC 2220
QY 2221 AGGATCCCTTAAGAGGCAACCTCCCTAGCGCCCTGCTGCTCATGTCACAGCGTGCAGG 2280
Db 2221 AGGATCCCTTAAGAGGCAACCTCCCTAGCGCCCTGCTGCTCATGTCACAGCGTGCAGG 2280
QY 2281 CCCCCAAGCCGAGTCTTCAAGCCTCTCTCATCACTGTCACAGCGTGCAGG 2340
Db 2281 CCCCCAAGCCGAGTCTTCAAGCCTCTCTCATCACTGTCACAGCGTGCAGG 2340
QY 2341 GCTCTGCTTCCCTGATAGTCTGCTGATCTGAGCTGAGAGCTTCGCTGCTGAGCT 2400
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 DEFINITION Sequence 2 from patent US 6475724.
 AR242745
 VERSION AR242745.1 GI:27289384
 KEYWORDS
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 ORGANISM Unknown.
 REFERENCE 1 (base 1 to 5304)
 AUTHORS Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.
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 Best Local Similarity 99.8%; Pred. No. 0;
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DB 4380 TTTATTAATTAACAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4439
QY 4440 ACTTGAATTAACAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4499
DB 4440 ACTTGAATTAACAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4499
QY 4500 AATTGATATTTGATTAATCATATTTCAATTAATTAATTAATTAATTAATTAATTAAT 4559
DB 4500 AATTGATATTTGATTAATCATATTTCAATTAATTAATTAATTAATTAATTAATTAAT 4559
QY 4560 TATATATTTGAAAACATTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4619
DB 4560 TATATATTTGAAAACATTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4619
QY 4620 GATGAG 4679
DB 4620 GATGAG 4679
QY 4680 ATGCAAG 4739
DB 4680 ATGCAAG 4739
QY 4740 GAGGGGGGAG 4799
DB 4740 GAGGGGGGAG 4799
QY 4800 CTTGCTGTTGAG 4859
DB 4800 CTTGCTGTTGAG 4859
QY 4860 TGAATTCAGATTTCTGAG 4919
DB 4860 TGAATTCAGATTTCTGAG 4919
QY 4920 GTGAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4979
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QY	361	ATGAGGACCAAAATTAATGAATAAGAAAAACAGCTCAGAAAAAAGATGTTCCAAATTGG	420
Dp	361	ATGAGGACCAAAATTAATGAATAAGAAAAACAGCTCAGAAAAAAGATGTTCCAAATTGG	420
QY	421	TAATTAAAGATTGTTCTTGGAAAGACCTCAGTAAGCTTGAATGGAAAATGGGAA	480
Dp	421	TAATTAAAGATTGTTCTTGGAAAGACCTCAGTAAGCTTGAATGGAAAATGGGAA	480
QY	481	AAACGTCAAAAGCATGATCTGATCAGATCCAAAGTATTAATTAAAAACCAT	540
Dp	481	AAACGTCAAAAGCATGATCTGATCAGATCCAAAGTATTAATTAAAAACCAT	540
QY	541	GGCATCATCTGGGAGAGCAAGTTGAGGAAAAGTCATGTTAGCAAAAGCATACAAATAC	600
Dp	541	GGCATCATCTGGGAGAGCAAGTTGAGGAAAAGTCATGTTAGCAAAAGCATACAAATAC	600
QY	601	AGCAAAATCAAAATTCGCAAAATGCAGAGAAAATGGGACTGGGAAAGCTTCAATAC	660
Dp	601	AGCAAAATCAAAATTCGCAAAATGCAGAGAAAATGGGACTGGGAAAGCTTCAATAC	660
QY	661	AGTATTTAGGCAAGTTAGCAAGTTGGCAACACTCCCTCTATACAGGGAACACAAA	720
Dp	661	AGTATTTAGGCAAGTTAGCAAGTTGGCAACACTCCCTCTATACAGGGAACACAAA	720
QY	721	ATTGACTGGGCTAAGCCTGACTTTCAAGGAAATATGAAAACTGAGACAAAACAAA	780
Dp	721	ATTGACTGGGCTAAGCCTGACTTTCAAGGAAATATGAAAACTGAGACAAAACAAA	780
QY	781	GACATGGTTAAAAGGCAACCAAGAACATTGTAGCCTTAAAGCAAGCTCCCTCAGCA	840
Dp	781	GACATGGTTAAAAGGCAACCAAGAACATTGTAGCCTTAAAGCAAGCTCCCTCAGCA	840
QY	841	GGGACCTGAGGCAATTTGCTTTAGGAGGCAAGTTCTTAAGAACTTTAAGAACTC	900
Dp	841	GGGACCTGAGGCAATTTGCTTTAGGAGGCAAGTTCTTAAGAACTTTAAGAACTC	900
QY	901	TTGAAATATATGAATTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACT	960
Dp	901	TTGAAATATATGAATTTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAACT	960
QY	961	TTTACATGAGGCTCCCAATTTTAAAGTCAGGCAATCAAGGATTAAGCTCCAGCTC	1020
Dp	961	TTTACATGAGGCTCCCAATTTTAAAGTCAGGCAATCAAGGATTAAGCTCCAGCTC	1020
QY	1021	GGATAGCTCAAAATCATTAAGAAATCACTGTGTCCCATCTTAATTTTCAAGAAATGATC	1080
Dp	1021	GGATAGCTCAAAATCATTAAGAAATCACTGTGTCCCATCTTAATTTTCAAGAAATGATC	1080
QY	1081	TGTCATGAGCCTCAGCAAGGAGGAGGTCAGCTCAACCAAGCAATCTACAAACCCA	1140
Dp	1081	TGTCATGAGCCTCAGCAAGGAGGAGGTCAGCTCAACCAAGCAATCTACAAACCCA	1140
QY	1141	GTGCTTCGAACATTGTTAAAGTGTATCTCAGTAAGATCCATTCAAAATGCCACTCCCTC	1200
Dp	1141	GTGCTTCGAACATTGTTAAAGTGTATCTCAGTAAGATCCATTCAAAATGCCACTCCCTC	1200
QY	1201	TGTGAGGCCATCCGCTCCACAGGAATCTCCCATCTTAAGCTTGTGATCAGATGT	1260
Dp	1201	TGTGAGGCCATCCGCTCCACAGGAATCTCCCATCTTAAGCTTGTGATCAGATGT	1260
QY	1261	TACAGCAGAAAGCTCCGTAAGGAGGAGGCTGTGTCTTAACACTTAACCTGTATGCTCTAC	1320
Dp	1261	TACAGCAGAAAGCTCCGTAAGGAGGAGGCTGTGTCTTAACACTTAACCTGTATGCTCTAC	1320
QY	1321	ACCTGAGCTCACTGCAACTCTGCTCCAGGTTCAAGCAATCTCTGTCAAGCTTCC	1380
Dp	1321	ACCTGAGCTCACTGCAACTCTGCTCCAGGTTCAAGCAATCTCTGTCAAGCTTCC	1380
QY	1381	CGGTAGCTGGGACATACAGGCGCAGCCGAGCTAAATTTTGTATTGTTAGTAAGAGATGGG	1440
Dp	1381	CGGTAGCTGGGACATACAGGCGCAGCCGAGCTAAATTTTGTATTGTTAGTAAGAGATGGG	1440
QY	1441	GTTTACCAATTAAGCCGAGCTGCTTTGAATCTTGAACCTCAGGCTGATCAACCAACTC	1500

Db	1441	GTTTACACATATTAGCCGGCTGGTCTTGAACCTCTGACCTCAGGTATCCACCACCTC	1500
Qy	1501	AGCCTCTTAAGTCTGGGATTACAGGCATGATGACCCGGCCGCAAGGTCAGTGT	1560
Db	1501	AGCCTCTTAAGTCTGGGATTACAGGCATGATGACCCGGCCGCAAGGTCAGTGT	1560
Qy	1561	TTATATAGGAATTAACCTTGATGGTTTACTTAACCAACAGGGGAAACACAAACCTGTGA	1620
Db	1561	TTATATAGGAATTAACCTTGATGGTTTACTTAACCAACAGGGGAAACACAAACCTGTGA	1620
Qy	1621	TAAATTCAAGGAATCTTGGGATGGGAAATGGTCATAGAGCTGCTGCTAGTCCAGAC	1680
Db	1621	TAAATTCAAGGAATCTTGGGATGGGAAATGGTCATAGAGCTGCTGCTAGTCCAGAC	1680
Qy	1681	CACCTGGTCTCATCACTTCTTCCCTCACTCACTCACTTTCAGGCTAAGTCACTTTTATT	1740
Db	1681	CACCTGGTCTCATCACTTCTTCCCTCACTCACTCACTTTCAGGCTAAGTCACTTTTATT	1740
Qy	1741	CACCACTGTTTGTGTAGCCTCCACATCGTTACTGAATTAAGATATACATTAACTAG	1800
Db	1741	CACCACTGTTTGTGTAGCCTCCACATCGTTACTGAATTAAGATATACATTAACTAG	1800
Qy	1801	TTCCATTGGGGCCCATCTGTGTGTGTATATAGGGGAGAGAGGCAATCCCAAGACTCT	1860
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Qy	1861	TGAAGCCCCCGGCAAGGTTCTCTCCAGCTGGGGAGCCTTGCAAGACCCGGGGTCC	1920
Db	1861	TGAAGCCCCCGGCAAGGTTCTCTCCAGCTGGGGAGCCTTGCAAGACCCGGGGTCC	1920
Qy	1921	TGGGTGCTGTAGAACCTGTGCACCCGGTCCACTGTTGTTTGTATCACTCTTAG	1980
Db	1921	TGGGTGCTGTAGAACCTGTGCACCCGGTCCACTGTTGTTTGTATCACTCTTAG	1980
Qy	1981	GACCTGTGCTTCTTATTTCTGTGTGACTGTGCATTCACAGGATTCATTTGCAATT	2040
Db	1981	GACCTGTGCTTCTTATTTCTGTGTGACTGTTCATTTCATTCAGGATTCATTTGCAATT	2040
Qy	2041	TATGAGTACTTATATCTGCCAAGACACACAGACAAATGTGTAGCAACGCTCATGCT	2100
Db	2041	TATGAGTACTTATATCTGCCAAGACACACAGACAAATGTGTAGCAACGCTCATGCT	2100
Qy	2101	CCTACCTTGTGAGTGAAGTTCATGTGATGAGAGCTGCAGAAAGAAATTAATATAGCA	2160
Db	2101	CCTACCTTGTGAGTGAAGTTCATGTGATGAGAGCTGCAGAAAGAAATTAATATAGCA	2160
Qy	2161	GCCAACTTAAACCCAGTCTGAAAGAAAGAAATTAACCACTTTGAAAGATTTGTGGC	2220
Db	2161	GCCAACTTAAACCCAGTCTGAAAGAAAGAAATTAACCACTTTGAAAGATTTGTGGC	2220
Qy	2221	AGCATCCCTTAAACAGGCACTCCCTAGGCCCCCTGTGCTGCATGTGCTCCGGAGG	2280
Db	2221	AGCATCCCTTAAACAGGCACTCCCTAGGCCCCCTGTGCTGCATGTGCTCCGGAGG	2280
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Db	2281	CCCCCAAGCCGAGTCTTCCAAAGCCTCTCTCCATCACTGTCACAGCGCTGACGTGGCT	2340
Qy	2341	GCCCTGCTTCCGATAGTCTGCTGTGATGTGAGCTGTGAGACCTCTTGCTGCTCAAGCT	2400
Db	2341	GCCCTGCTTCCGATAGTCTGCTGTGATGTGAGCTGTGAGACCTCTTGCTGCTCAAGCT	2400
Qy	2401	CCAGAAAGGAATGAGAGGGAACCTAGTCTAAGGGAATCTTGAGGGGACAGTGTTC	2460
Db	2401	CCAGAAAGGAATGAGAGGGAACCTAGTCTAAGGGAATCTTGAGGGGACAGTGTTC	2460
Qy	2461	CTCAGAGGGGAGGGGCTCCACATCTCCAGAGAAATTCAGAGAGGTGGGGAATGAGGGAG	2520
Db	2461	CTCAGAGGGGAGGGGCTCCACATCTCCAGAGAAATTCAGAGAGGTGGGGAATGAGGGAG	2520
Qy	2521	TGGGAGCGCTGGGCTGAGCGGGTCTGAAGGCGAGAGGTGAAAAGGGCAAGCTGAA	2580

Db 2521 TGCGGACCGCTGGGGCTGACCGCGTGTGAAAGGACGAGAGGTGAAAAGGCAAGCTGAA 2580
 QY 2581 GCTGCCGATGTTCAAGTGTGTTTCAAGGGGCTGGAGATTTCCTGCTGCTGCTGAGC 2640
 Db 2581 GCTGCCGATGTTCAAGTGTGTTTCAAGGGGCTGGAGATTTCCTGCTGCTGCTGAGC 2640
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 Db 2641 CTTTATCTTTCTCTGCTGGAGAGAAAGTCTATTTCATGAGAGGAGTTC 2700
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 Db 2701 ATAAAGTACGCTGTTAAATTCAGGGGTGACATGGGTTTCTTCAAGAGCCTTAT 2760
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 Db 2881 TGCAGAGCGTGCAGAAACCTTGAAATCAGAGAGTGGGTTTCTTCTGAGTGAAT 2940
 QY 2941 GGTGGCTGTGAGACCGTGGCAAGTCTTCTCTCTCTGAGCAATGCTTCTCTGCT 3000
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 QY 3181 CAGACGAGAGGAGAGAGCTGAGAGAGCTGAGAGAGCTGAGAGAGCTGAGAGAG 3240
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 QY 3541 GTTCTAG 3600
 Db 3541 GTTCTAG 3600
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 QY 3721 GAGATTCAG 3780
 Db 3721 GAGATTCAG 3780
 QY 3781 TAAAGCAAGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3840
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 Db 3961 AGAATGAGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 4020
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 Db 4081 TGCTCAAG 4140
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 QY 4501 ATTGGAATTAAG 4560
 Db 4501 ATTGGAATTAAG 4560
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 Db 4561 ATATATTAAG 4620
 QY 4621 CATGCAACAG 4680
 Db 4621 CATGCAACAG 4680
 QY 4681 TGCAAG 4740
 Db 4681 TGCAAG 4740

[illegible]

RESULT 2
 US-08-938-669A-3
 Sequence 3, Application US/08938669A
 Patent No. 6171788
 GENERAL INFORMATION:
 APPLICANT: Nguyen, Thai D.
 APPLICANT: Polansky, Jon R.
 TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
 TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
 TITLE OF INVENTION: RELATED DISEASES
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Howrey & Simon
 STREET: 1299 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20004-2402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/938,669A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/791,154
 FILING DATE: 28-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Mendelson, Elliot
 REGISTRATION NUMBER: P-42,878
 REFERENCE/DOCKET NUMBER: 07425-0034
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202 383-6857

TELEFAX: 202 383-6610
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6169 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-538-669A-3

Query Match	100.0%;	Score 5271;	DB 3;	Length 6169;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 5271; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

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Dp	61	TCCATATACTGATAGCTCCATTCGATGATATGTCCTTGGCAGAGATGATTAAGATCA	120
QY	121	GGAAGAAGAGATATCCAGTTAGCCAGAGTCCAGGCTGTGTCTGCTTATTTTATGTA	180
Dp	121	GGAAGAAGAGATATCCAGTTAGCCAGAGTCCAGGCTGTGTCTGCTTATTTTATGTA	180
QY	181	CAGATGTTGCTCTGACAGAGCTATCTTCAGGAAACATCAGATCCAAATGGAATC	240
Dp	181	CAGATGTTGCTCTGACAGAGCTATCTTCAGGAAACATCAGATCCAAATGGAATC	240
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Dp	241	CATCAAAACAGAGCTTAAGAAACAGGATGAGATGGGCACTTGCCCAAGSAAAAATGCGAG	300
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Dp	661	AGTGAATTAGGCAAGTTGACATGTTGCAACACTCCCGCTTATACGAGGAACAATAA	720
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Dp	721	ATTGACTGGGCTTAAGCTTGACATTTCAAGGSAATATGAAAAACTGAGCAAAAATAA	780
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Dp	841	GGGAGCCCTGAGCATTTGCTTTAGAAAGGCGAGTCTTTCTTAAGAACTTTAAGAACTC	900

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Db 2221 AGCATCCCTTAACAGGCGCACTCCCTGAGCGCCCTGTGTGTGTGTGTGTGTGTGTGTGT 2280
QY 2281 CCCCAGCCGAGTCTTCCAGGCTCTCTCTCAATCACTCAAGCTGTGTGTGTGTGTGTGTGT 2340
Db 2281 CCCCAGCCGAGTCTTCCAGGCTCTCTCTCAATCACTCAAGCTGTGTGTGTGTGTGTGTGT 2340
QY 2341 GCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400
Db 2341 GCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400
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Db 2461 CTGAGAGGAAAGGAGGCTTCAAGCTCAAGAGAAATTTCCAGAGAGTGTGTGTGTGTGT 2520
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Db 2521 TGGGAGCGTGGAGGCTGTGAGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2580
QY 2581 GCTGCCAGATGTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2640
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QY 3061 GGATGTTAAGAGGAGGAGGAGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3120
Db 3061 GGATGTTAAGAGGAGGAGGAGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3120
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[illegible]

RESULT 3 US-09-306-828-3

Sequence 3, Application US/09306828
Patent No. 6475724
GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
APPLICANT: Chen, Pu
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
CURRENT APPLICATION NUMBER: US/09/306,828
CURRENT FILING DATE: 1999-05-07
EARLIER APPLICATION NUMBER: US 09/227,881
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Word 97
SEQ ID NO: 3
LENGTH: 6169
TYPE: DNA
ORGANISM: Homo sapiens
US-09-306-828-3

Query Match 100.0%; Score 5271; DB 4; Length 6169;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCTTGTCTAGTTTACCTCAGGCGCTATTATGAATGAATGAGATACCAATGTGAAG 60
DB 1 ATCTTGTCTAGTTTACCTCAGGCGCTATTATGAATGAATGAGATACCAATGTGAAG 60
QY 61 TCTATTAACCTGTAAGCTCTCCATTCGGATGTAATGCTTTGGCAGAGATGAAGAATCA 120
DB 61 TCTATTAACCTGTAAGCTCTCCATTCGGATGTAATGCTTTGGCAGAGATGAAGAATCA 120
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DB 121 GGAAGAAAGAGTATCCAGCTTGAAGCAAGTGCAGAGCTGTGCTGCTTATTTTGA 180
QY 121 GGAAGAAAGAGTATCCAGCTTGAAGCAAGTGCAGAGCTGTGCTGCTTATTTTGA 180
DB 121 GGAAGAAAGAGTATCCAGCTTGAAGCAAGTGCAGAGCTGTGCTGCTTATTTTGA 180
QY 181 CAGATGTTGCTCCTGACAGAGCTATTCTCAGGAAACATCACATATGTAATC 240
DB 181 CAGATGTTGCTCCTGACAGAGCTATTCTCAGGAAACATCACATATGTAATC 240
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DB 241 CATCAACAGAGCTTAAGAAACAGAGATGAGATGAGGACTTGGCCCAAGGAAATGCCAG 300
QY 241 CATCAACAGAGCTTAAGAAACAGAGATGAGATGAGGACTTGGCCCAAGGAAATGCCAG 300
DB 241 CATCAACAGAGCTTAAGAAACAGAGATGAGATGAGGACTTGGCCCAAGGAAATGCCAG 300
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DB 301 GAGAGCAATATGATGATGAATAATACTTTCCCTTGTATTTTATTTTCAAGAAAAATG 360
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DB 361 ATGAGGACCAAAATCAATGAATGAAGAAAAAGCTGACGAAAAAGATGTTTCCAAATTGG 420
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DB 601 AGCAAAATCAAAATTTCCGCAATGAGAGGAAATGGGAGCTGGGAAAGCTTCAATTAAC 660
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DB 661 AGTGAATGAGGAGTTGACCAATGTTTCCGCAACCTTCCCGTCTAATACAGGAAACAGAAA 720
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DB 721 ATTGACGTGGCTAAGCTGCTGATCTTCAAGGAAATATGAAAACTGAGAGCAAAACAAA 780
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DB 781 GACATGGTTAAAGGCAACAGAACTTGTGAGCTTCAAGCAGAGTGCCTTCAGCA 840
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DB 841 GGAACCTGTGAGGATTTGCTTGAAGAGGAGGAGTTTCTTAAGGATTTTGAAGAACTC 900
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QY 961 TTTAGCATGGTCCCAATTTTAAAGTCAAGCATTAAGATTAAGTCCAGCTCC 1020
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DB 1021 GGATAGGTCAGAAATCATTTGAATGATCTGTGCCCATCTTAATCTTTTCAAGATGATC 1080
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DB 1081 TGTCAATAGCCCTCACAACAGAGCCGATGTGTGACTTAACAACATCTCAACCCAA 1140
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DB 1501 AGCCTCTAAAGTGTGAGGATTAACAGGATGATCAACCGCCGCGCAAGGGTCAAGT 1560
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QY 1681 CACTGCTCTATCACTTTCTTCCCTATCTCAATTTTCAAGGCTTAAGTATTAAT 1740
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Qy 1861 TGAAGCCCCGGAGAGAGTTTCTCTCCAGCTGGGGAGCCCTGCAAGCAACCCGGGCTCC 1920
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Qy 1921 TGGGTGTCTGAGCAACCTGCGACGCCCGGTGCACTGTGTGTTTGTATCACTCTAGS 1980
Db 1921 TGGGTGTCTGAGCAACCTGCGACGCCCGGTGCACTGTGTGTTTGTATCACTCTAGS 1980
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 DB 4621 CATGACACACACAGAGTATGAAAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 4680
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 DB 4681 TGCAAGACTGAAATTAAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 4740
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 QY 4861 GGATCTCCAGTCTTCCAGATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4920
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 QY 4981 TGAATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5040
 DB 4981 TGAATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5040
 QY 5041 TGAAGACTTATTTGAGGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 5100
 DB 5041 TGAAGACTTATTTGAGGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 5100

DB 5041 TGAAGACTTATTTGAGGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTG 5100
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 DB 5161 CCGTGCAGAGGCCCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 5220
 QY 5221 GCTCCCACTATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5271
 DB 5221 GCTCCCACTATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5271

RESULT 4
 US-08-938-669A-1
 Sequence 1, Application US/08938669A
 Patent No. 6171788
 GENERAL INFORMATION:
 APPLICANT: Nguyen, Thai D.
 APPLICANT: Polansky, Jon R.
 TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS, PROGNOSIS, AND TREATMENT OF GLAUCOMA AND
 TITLE OF INVENTION: RELATED DISEASES
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSES: Howrey & Simon
 STREET: 1299 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20004-2402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSBO for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/938,669A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/791,154
 FILING DATE: 28-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Mendelson, Elliot
 REGISTRATION NUMBER: P-42,878
 REFERENCE/DOCKET NUMBER: 07425-0034
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202 383-6857
 TELEFAX: 202 383-6610
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5300 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-938-669A-1

Query Match 99.5%; Score 5246.4; DB 3; Length 5300;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 5269; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 ATCTTTGTCAGTTTACCTCAAGGCTATTAAGAAATGAATGAATGAATGAATGAATGAATGA 60
 DB 1 ATCTTTGTCAGTTTACCTCAAGGCTATTAAGAAATGAATGAATGAATGAATGAATGAATGA 60
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RESULT 5
US-09-306-828-1
Sequence 1, Application US/09306828
Patent No. 6475724
GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
APPLICANT: Chen, Pu
APPLICANT: Chen, Hu
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
CURRENT APPLICATION NUMBER: US/09/306,828
CURRENT FILING DATE: 1999-05-07
EARLIER APPLICATION NUMBER: US 09/227,881
EARLIER FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Word 97
SEQ ID NO 1
LENGTH: 5300
TYPE: DNA

ORGANISM: Homo sapiens
US-09-306-828-1
Query Match 99.5%; Score 5246.4; DB 4; Length 5300;
Base Local Similarity 99.9%; Pred. No. 0;
Matches 5269; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
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Dp	2341	GCTGAGCTCCCGTGAATCGCTCTGAGCACTGAGCTGAGCACTCTTGCTCCAGCT	2400
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Dp	2701	ATAAAGTCAAGCTGTAAATATCCAGGGTGTGACTGGGTTTTCCTTACAGAGCCCTTAT	2760
Qy	2761	TTAATGGGAATATAGAAAGCGAGCTCAATTTCTTAGGCGCTTAATTCACGAAAGATGAC	2820
Dp	2761	TTAATGGGAATATAGAAAGCGAGCTCAATTTCTTAGGCGCTTAATTCACGAAAGATGAC	2820
Qy	2821	TGAGAGCTTTTCTTTCATAGTCTTCTGGGCAACTACTCAGGCCGTGTGGAATTGAGCTTA	2880
Dp	2821	TGAGAGCTTTTCTTTCATAGTCTTCTGGGCAACTACTCAGGCCGTGTGTGGAATTGAGCTTA	2880
Qy	2881	TGCAAGAGCGTGCAAAACCTTGAATCAGAGACTCGATTTCCTTCTGCTTCTGCCATT	2940
Dp	2881	TGCAAGAGCGTGCAAAACCTTGAATCAGAGACTCGATTTCCTTCTGCTTCTGCCATT	2940
Qy	2941	GGTGGAGCTGTGAGACCGTGGCAAGTGTCTCTTCCCTGGGGCACTACTCTTCTCTCT	3000
Dp	2941	GGTGGAGCTGTGAGACCGTGGCAAGTGTCTCTTCCCTGGGGCACTACTCTTCTCTCT	3000
Qy	3001	ATTAAGACCTTTCAGCTCTGTGTCTTGTGAACACTTCCCTGTGATTCTCTGTGAGGG	3060
Dp	3001	ATTAAGACCTTTCAGCTCTGTGTCTTGTGAACACTTCCCTGTGATTCTCTGTGAGGG	3060
Qy	3061	GGATGTTGAGAGGGAGAGAGCAGAGACTTGAGCACTGAGCCAAGGGAGGTGAGGG	3120
Dp	3061	GGATGTTGAGAGGGAGAGAGCAGAGACTTGAGCACTGAGCCAAGGGAGGTGAGGG	3120
Qy	3121	GGAACGAAAGGAGGCAAGGCTGGGTGTCTCATAGTCTCTCACTGATCACTCAGATTC	3180
Dp	3121	GGAACGAAAGGAGGCAAGGCTGGGTGTCTCATAGTCTCTCACTGATCACTCAGATTC	3180

3181 CAGGACCGAGAGCCACATGCTTCAGGAAAGCTCAATGAAACCCACAGCAGCATTTCTCT 3240
Db 3181 CAGGACCGAGAGCCACATGCTTCAGGAAAGCTCAATGAAACCCACAGCAGCATTTCTCT 3240
Qy 3241 TCCCTAAGCATTAAGCATTTGGCATTTCGCAATACCAAAAAAGATGACAGACTAATCTGCT 3300
Db 3241 TCCCTAAGCATTAAGCATTTGGCATTTCGCAATACCAAAAAAGATGACAGACTAATCTGCT 3300
Qy 3301 GGTAGCTTTTGCCTGCAATCAAAAACTGGGCGCAGACAGTGAATAATGTCAGAGATTG 3360
Db 3301 GGTAGCTTTTGCCTGCAATCAAAAACTGGGCGCAGACAGTGAATAATGTCAGAGATTG 3360
Qy 3361 TTAAACTTTTCCCTGACCCGACAGACCCACAGCAGCTCAAGAGTGAATGTCAGAGATTG 3420
Db 3361 TTAAACTTTTCCCTGACCCGACAGACCCACAGCAGCTCAAGAGTGAATGTCAGAGATTG 3420
Qy 3421 AGTACCTGACGCGCAGAGGAG 3480
Db 3421 AGTACCTGACGCGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3480
Qy 3481 ACAGATTCATTCAAGGCGAGGTGGAAATTGACACAGAGGATTATAGTCCACGTCGATCTGG 3540
Db 3481 ACAGATTCATTCAAGGCGAGGTGGAAATTGACACAGAGGATTATAGTCCACGTCGATCTGG 3540
Qy 3541 GTTCTAGAGGCGAGGCTATATTTGAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3600
Db 3541 GTTCTAGAGGCGAGGCTATATTTGAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3600
Qy 3601 CCTGATTTCTAATACTAATAATTTTCTTTACAGCTGAGTAATTTCTGACAGTCAACAG 3660
Db 3601 CCTGATTTCTAATACTAATAATTTTCTTTACAGCTGAGTAATTTCTGACAGTCAACAG 3660
Qy 3661 GTAGTAACGAGGCTGATAGATTACTAGATTCTCTCTTATAGAACTCTTTTCTCTCT 3720
Db 3661 GTAGTAACGAGGCTGATAGATTACTAGATTCTCTCTTATAGAACTCTTTTCTCTCT 3720
Qy 3721 GAGATGAGAGACACAGGCGCAATCCGTTCTTTACAGAGAGAGAGAGAGAGAGAGAGAG 3780
Db 3721 GAGATGAGAGACACAGGCGCAATCCGTTCTTTACAGAGAGAGAGAGAGAGAGAGAGAG 3780
Qy 3781 TAAAGCCAAACAGATTCAAGCTTAGCTTGTGCTGATATAGATTGTTTTGAAAAAT 3840
Db 3781 TAAAGCCAAACAGATTCAAGCTTAGCTTGTGCTGATATAGATTGTTTTGAAAAAT 3840
Qy 3841 CATTCAGGATGTTTACTATCTGATTCAGAAAAATGAGACTAGAACCTTTGGTCAAGCTG 3900
Db 3841 CATTCAGGATGTTTACTATCTGATTCAGAAAAATGAGACTAGAACCTTTGGTCAAGCTG 3900
Qy 3901 TAAACAAACACCCAGTTGTAATGTTCAAGTTCAAGGCTTAAGTCAAGAACCAATCAAA- 3959
Db 3901 TAAACAAACACCCAGTTGTAATGTTCAAGTTCAAGGCTTAAGTCAAGAACCAATCAAA- 3959
Qy 3960 AAGAAATAGAACTTTAGAGCAAACTGTTCTCCACACTGAGAGGTGATCTGCCAGG 4019
Db 3961 AAGAAATAGAACTTTAGAGCAAACTGTTCTCCACACTGAGAGGTGATCTGCCAGG 4019
Qy 4020 CAGTTGGAATATTTACTTCAAGATATGACACTGTTGTTGTTATTAACAATTAAG 4079
Db 4020 CAGTTGGAATATTTACTTCAAGATATGACACTGTTGTTGTTATTAACAATTAAG 4079
Qy 4080 TTGCTCAAGAGAACTATTTTCAAGTGGCTTAAAGTACTCTGACAGCTTTGGTAATA 4139
Db 4080 TTGCTCAAGAGAACTATTTTCAAGTGGCTTAAAGTACTCTGACAGCTTTGGTAATA 4139
Qy 4140 TTTATTTGCTATTGCTATTGCTTTTGTTTTCTCTTTGGGTTTATTAAGTAAAGA 4199
Db 4140 TTTATTTGCTATTGCTATTGCTTTTGTTTTCTCTTTGGGTTTATTAAGTAAAGA 4199
Qy 4200 GGGATTATTAACCTTAAGCTCAAGAAAGCTGTGAATTTGAATGAGAGAAAAATTAATTT 4259
Db 4200 GGGATTATTAACCTTAAGCTCAAGAAAGCTGTGAATTTGAATGAGAGAAAAATTAATTT 4259
Qy 4260 TTGTTTACACCTTTAACTAATTTAACTTTATTTGCAATTGGGAATAGAGCATTA 4319

4260 TTTGTTTACACCTTTCTAATAATTTTAACTTTTATTCATTTGCGAATAGAGCCATTA 4319
Db 4260 TTTGTTTACACCTTTCTAATAATTTTAACTTTTATTCATTTGCGAATAGAGCCATTA 4319
Qy 4320 ACTCAAGGTGAATTAACAGTACTGTGAATTTTGCATTACCAATAGAAATCAGAGCAT 4379
Db 4320 ACTCAAGGTGAATTAACAGTACTGTGAATTTTGCATTACCAATAGAAATCAGAGCAT 4379
Qy 4380 TTTATCTATATTAAGTGTGAGATAGAGTGAATGAATAATTTATCTAAACT 4439
Db 4380 TTTATCTATATTAAGTGTGAGATAGAGTGAATGAATAATTTATCTAAACT 4439
Qy 4440 ACTTTGAAAATGAGCTCTGCTGATCTGTTTAACTAATTAATTAACATGTTAA 4499
Db 4440 ACTTTGAAAATGAGCTCTGCTGATCTGTTTAACTAATTAATTAACATGTTAA 4499
Qy 4500 AATTTGGAATTTTGAATTAATTAATTTTATTAATTTTCTTTGTTATTAATTT 4559
Db 4500 AATTTGGAATTTTGAATTAATTAATTTTATTAATTTTCTTTGTTATTAATTT 4559
Qy 4560 TATATATTTGAAAACATCTTTCTGAGAGAGTCCCAAGATTTTCAACCAATGAGGTTG 4619
Db 4560 TATATATTTGAAAACATCTTTCTGAGAGAGTCCCAAGATTTTCAACCAATGAGGTTG 4619
Qy 4620 GCATGCAACACACAGAGTAAAGCTGATTTAGAGCTTAACATTGACATTGTCCTGAG 4679
Db 4620 GCATGCAACACACAGAGTAAAGCTGATTTAGAGCTTAACATTGACATTGTCCTGAG 4679
Qy 4680 ATGCAAGCTGAATTTAAGAGTCTCCCAAGATTAACAGTGTTTTAAAGCTAGGGGT 4739
Db 4680 ATGCAAGCTGAATTTAAGAGTCTCCCAAGATTAACAGTGTGTTTTAAAGCTAGGGGT 4739
Qy 4740 GAGGGGGGAAAATCTGCGCTTTCTATAGAAATGCTCTCTGAGAGCTGTAGGGTCTGT 4799
Db 4740 GAGGGGGGAAAATCTGCGCTTTCTATAGAAATGCTCTCTGAGAGCTGTAGGGTCTGT 4799
Qy 4800 CCTGTGTTCTGCGCTGCTGATTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4859
Db 4800 CCTGTGTTCTGCGCTGCTGATTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4859
Qy 4860 TEGATCTCAGTTCCTAGCAATGAGCTGACAGAGTGCAGAGTCTCAATGAGTTTSCAGA 4919
Db 4860 TEGATCTCAGTTCCTAGCAATGAGCTGACAGAGTGCAGAGTCTCAATGAGTTTSCAGA 4919
Qy 4920 GTGAATGGAATATTAACCTAGAAATATATCTTGTGAAATCAGCACACCAAGTATCTG 4979
Db 4920 GTGAATGGAATATTAACCTAGAAATATATCTTGTGAAATCAGCACACCAAGTATCTG 4979
Qy 4980 GTGTAAAGTGTGTAAGT 5039
Db 4980 GTGTAAAGTGTGTAAGT 5039
Qy 5040 ATAGAACTATTAATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAG 5099
Db 5040 ATAGAACTATTAATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAG 5099
Qy 5100 CCAACAGACTCTGGAAGGTTATTTTCTAAGAACTGTGCTGAGAGGAGGAGGAGGAGGAG 5159
Db 5100 CCAACAGACTCTGGAAGGTTATTTTCTAAGAACTGTGCTGAGAGGAGGAGGAGGAGGAG 5159
Qy 5160 CCTGTGCAACAGCCCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAG 5219
Db 5160 CCTGTGCAACAGCCCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAG 5219
Qy 5220 GGGTCCCAAGTATTAATTAATCTCTGAGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 5271
Db 5220 GGGTCCCAAGTATTAATTAATCTCTGAGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 5271

RESULT 6
US-08-669A-2
; Sequence 2, Application US/08938669A
; Parent No. 6171788
; GENERAL INFORMATION:

APPLICANT: Nguyen, Thai D.
 APPLICANT: Polansky, Jon R.
 TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
 TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
 TITLE OF INVENTION: RELATED DISEASES
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Howrey & Simon
 STREET: 1299 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20004-2402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/938,669A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/791,154
 FILING DATE: 28-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Mendelson, Elliot
 REGISTRATION NUMBER: P-42,878
 REFERENCE/DOCKET NUMBER: 07425-0034
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202 383-6857
 TELEFAX: 202 383-6610
 TELEX:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5304 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-938-669A-2

Query Match 99.1%; Score 5224.4; DB 3; Length 5304;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 5264; Conservative 0; Mismatches 6; Indels 6; Gaps 3;

QY 1 ATCTTTGTCAGTTTACCTCAGGCTATTATGAAATGAAATGAGATTAACCAATGTGAAAG 60
 DB 1 ATCTTTGTCAGTTTACCTCAGGCTATTATGAAATGAAATGAGATTAACCAATGTGAAAG 60
 QY 61 TCCATTAACCTGTAAGCTTCATTCGGATGATGCTTTGGCAGAGATGATAAGATA 120
 DB 61 TCCATTAACCTGTAAGCTTCATTCGGATGATGCTTTGGCAGAGATGATAAGATA 120
 QY 121 GGAAGAAGAGATCAAGCTTAGCCAGTGTCCAGCTGTCTGTCTTATTTTGTGA 180
 DB 121 GGAAGAAGAGATCAAGCTTAGCCAGTGTCTGTCTGTCTTATTTTGTGA 180
 QY 181 CAGATGTTGCTCTGACAGAAAGCTATTCTTCAGGAAAATCATCATCCAAATGTAATC 240
 DB 181 CAGATGTTGCTCTGACAGAAAGCTATTCTTCAGGAAAATCATCATCCAAATGTAATC 240
 QY 241 CATCAACAGAGAGCTTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGAAAATGCGAG 300
 DB 241 CATCAACAGAGAGCTTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGAAAATGCGAG 300
 QY 301 GAGAGCAATATATGATGAAAAATTAACCTTTCCCTTTGTTTAAATTCAGAAAAATG 360
 DB 301 GAGAGCAATATATGATGAAAAATTAACCTTTCCCTTTGTTTAAATTCAGAAAAATG 360
 QY 361 ATGAGAGCAATATATGATGAAAAATGAGAAACAGCTCGAAGAAAATGATGTTTCAAAATGG 420
 DB 361 ATGAGAGCAATATATGATGAAAAATGAGAAACAGCTCGAAGAAAATGATGTTTCAAAATGG 420

QY 421 TAATTAAGTATTGTTCCCTTGGAAGAGACCTTCATGTGAGCTGATGGGAAAATGGGA 480
 DB 421 TAATTAAGTATTGTTCCCTTGGAAGAGACCTTCATGTGAGCTGATGGGAAAATGGGA 480
 QY 481 AATCGTCAAGAGATATCTGATCGATCCCAATGAGATTAATTTTAAACACAGAT 540
 DB 481 AATCGTCAAGAGATATCTGATCGATCCCAATGAGATTAATTTTAAACACAGAT 540
 QY 541 GGCATCACTCTGGGAGAGCAAGTTGAGAAAGTCAATGTTAGCAAGGACATTAACATAAC 600
 DB 541 GGCATCACTCTGGGAGAGCAAGTTGAGAAAGTCAATGTTAGCAAGGACATTAACATAAC 600
 QY 601 AGCAAAATCAAAATTTCCGAATGACAGAGGAAAAATGGGAGCTGGGAAAAGCTTATAC 660
 DB 601 AGCAAAATCAAAATTTCCGAATGACAGAGGAAAAATGGGAGCTGGGAAAAGCTTATAC 660
 QY 661 AGTGAATGAGCAGTTGACCATGTTGCAACACCTCCCGCTATACAGGGAACACAAA 720
 DB 661 AGTGAATGAGCAGTTGACCATGTTGCAACACCTCCCGCTATACAGGGAACACAAA 720
 QY 721 ATTGACTGGCTAAGCCTGGAATTTGAGAAAGCCAGTTTCTTAAGAAATCTTAAGAACTC 780
 DB 721 ATTGACTGGCTAAGCCTGGAATTTGAGAAAGCCAGTTTCTTAAGAAATCTTAAGAACTC 780
 QY 781 GACATGTTTAAAGGAGAACAGAACATTTGAGCCCTTCAAGCAGAGAGCCCTCAGCA 840
 DB 781 GACATGTTTAAAGGAGAACAGAACATTTGAGCCCTTCAAGCAGAGAGCCCTCAGCA 840
 QY 841 GGAACCTGAGGATTTGCTTTAGAAAGCCAGTTTCTTAAGAAATCTTAAGAACTC 900
 DB 841 GGAACCTGAGGATTTGCTTTAGAAAGCCAGTTTCTTAAGAAATCTTAAGAACTC 900
 QY 901 TTGAAGATCATGATTTTAAACATTTTAAAGTAAACAAATATGCGATGATATCAG 960
 DB 901 TTGAAGATCATGATTTTAAACATTTTAAAGTAAACAAATATGCGATGATATCAG 960
 QY 961 TTTGAGATGAGTCCCAATTTTAAAGCAGGATCAAGAAAGTAAAGTAAAGTAAAGTAAAG 1020
 DB 961 TTTGAGATGAGTCCCAATTTTAAAGCAGGATCAAGAAAGTAAAGTAAAGTAAAGTAAAG 1020
 QY 1021 GGATAGGTCAGAAATCATGAAATCATGTCCTCCCATCTTAACCTTTTCAGATGATC 1080
 DB 1021 GGATAGGTCAGAAATCATGAAATCATGTCCTCCCATCTTAACCTTTTCAGATGATC 1080
 QY 1081 TGTATAGCCCTCAGACAGAGCCAGTGTGTGACCTTAACCAACATCTACACCA 1140
 DB 1081 TGTATAGCCCTCAGACAGAGCCAGTGTGTGACCTTAACCAACATCTACACCA 1140
 QY 1141 GTGCTCAACCATTTGATAGTGTCAATCTCAGTATGCTTCAATTAACAAATGCCACTCC 1200
 DB 1141 GTGCTCAACCATTTGATAGTGTCAATCTCAGTATGCTTCAATTAACAAATGCCACTCC 1200
 QY 1201 TGTGAGGCCATCCCGCTCCACAGAAAGTCTCCCATCTAGACCTTGTGATAGAGATG 1260
 DB 1201 TGTGAGGCCATCCCGCTCCACAGAAAGTCTCCCATCTAGACCTTGTGATAGAGATG 1260
 QY 1261 TACAGCCAGAAAGCTCCGTGAGAGGAGTGTGTCTTACACCTTACTGTATGCTTAC 1320
 DB 1261 TACAGCCAGAAAGCTCCGTGAGAGGAGTGTGTCTTACACCTTACTGTATGCTTAC 1320
 QY 1321 ACCTGAGCTCACTGCAACCTCTGCTCCAGGTTCAAGCAATCTCTGTCTAGGCTCC 1380
 DB 1321 ACCTGAGCTCACTGCAACCTCTGCTCCAGGTTCAAGCAATCTCTGTCTAGGCTCC 1380
 QY 1381 CGCGTGTGGAATTAAGAGGCGAGCGCCGCTAATTTTGTATGTTAGTAAAGATGG 1440
 DB 1381 CGCGTGTGGAATTAAGAGGCGAGCGCCGCTAATTTTGTATGTTAGTAAAGATGG 1440
 QY 1441 GTTTCACCATTAAGCCCGGTGTCTTGAATCTCTGACCTCAGTGTATCACCACCTC 1500
 DB 1441 GTTTCACCATTAAGCCCGGTGTCTTGAATCTCTGACCTCAGTGTATCACCACCTC 1500
 QY 1501 AGCTCTTAAGTGTCTGGAATTAAGGCAATGATCACCGGCGCCGCAAGGGTCAAGTGT 1560

Db 1501 AGCTCTTAAGTCTGGATTAAGGACGATGACCGGCGCCAGGAGTCAAGTCT 1560
Qy 1561 TTAATTAAGAACTACTGAAATGCTTTACTTAACCAACAGGAAACAGACAAAAGCTGGA 1620
Db 1561 TTAATTAAGAACTACTGAAATGCTTTACTTAACCAACAGGAAACAGACAAAAGCTGGA 1620
Qy 1621 TAATTTAGAGGATTTCTGGATGGGAAATGTCGCCATGAGCTGCTGCTAGTCCCAAC 1680
Db 1621 TAATTTAGAGGATTTCTGGATGGGAAATGTCGCCATGAGCTGCTGCTAGTCCCAAC 1680
Qy 1681 CACTGCTCTCATCATCTTTTCTCCCTCATCTTCATTTTCAAGCTAAAGTTACATTTAT 1740
Db 1681 CACTGCTCTCATCATCTTTTCTCCCTCATCTTCATTTTCAAGCTAAAGTTATTTAT 1740
Qy 1741 CACCATCTTTTGTGTGAAGCTTCCATCGTGTACTGAAATTAAGTATPACATAAGCTAG 1800
Db 1741 CACCATCTTTTGTGTGAAGCTTCCATCGTGTACTGAAATTAAGTATPACATAAGCTAG 1800
Qy 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGAGAGAGGACATACCCAGAGACTCT 1860
Db 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGAGAGAGGACATACCCAGAGACTCT 1860
Qy 1861 TGAAGCCCGGAGAGGTTTCTCTCCAGCTGGGGAGCCCTGACACCCCGGGTCC 1920
Db 1861 TGAAGCCCGGAGAGGTTTCTCTCCAGCTGGGGAGCCCTGACACCCCGGGTCC 1920
Qy 1921 TGGGTGTCTGAGCAACTGTGCAGCCCGTGCACATGTTTGTATCACTCTAG 1980
Db 1921 TGGGTGTCTGAGCAACTGTGCAGCCCGTGCACATGTTTGTATCACTCTAG 1980
Qy 1981 GACCTGTGTCTTCTATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
Db 1981 GACCTGTGTCTTCTATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
Qy 2041 TATTGATCTTATCTGCTCAGACACAGACAAAATGAGCAAGAGAGTCACTGC 2100
Db 2041 TATTGATCTTATATCTGCTCAGACACAGACAAAATGAGCAAGAGAGTCACTGC 2100
Qy 2101 CCTACTTGTGTGAGGTGACAGTTTCTCATGAGAGAGTGCAGAAATTAATAGCCA 2160
Db 2101 CCTACTTGTGTGAGGTGACAGTTTCTCATGAGAGAGTGCAGAAATTAATAGCCA 2160
Qy 2161 GCCAATTTAAACCCAGTGTGTAAGAAAGAAATTAACCATCTGAAAGTTGTGCGC 2220
Db 2161 GCCAATTTAAACCCAGTGTGTAAGAAAGAAATTAACCATCTGAAAGTTGTGCGC 2220
Qy 2221 AGCATCTTTAAACAGGCCACCTCCCTAGCGCCCTGCTGCTGCATCGTGCCTGAGG 2280
Db 2221 AGCATCTTTAAACAGGCCACCTCCCTAGCGCCCTGCTGCTGCATCGTGCCTGAGG 2280
Qy 2281 CCCCCAAGCCGAGTCTTCCAGCCTCTCTCCATGAGTCAAGCGCTGAGTGGCCT 2340
Db 2281 CCCCCAAGCCGAGTCTTCCAGCCTCTCTCCATGAGTCAAGCGCTGAGTGGCCT 2340
Qy 2341 GCTCTGCTTCCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400
Db 2341 GCTCTGCTTCCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400
Qy 2401 CCAGAAAGAAATGAGAGGAAATAGTCTTACGAGAAATCTGAGAGGAGCAAGTGTTC 2460
Db 2401 CCAGAAAGAAATGAGAGGAAATAGTCTTACGAGAAATCTGAGAGGAGCAAGTGTTC 2460
Qy 2461 CTCAAGAGGAGGAGGCTCCAGCTCCAGAGAAATTCAGAGAGTGGGAGCTGAGAGAG 2520
Db 2461 CTCAAGAGGAGGAGGCTCCAGCTCCAGAGAAATTCAGAGAGTGGGAGCTGAGAGAG 2520
Qy 2521 TGGGAGCGTGGGCTGAGCGGCTGTAAGAGGAGAGAGTGAAGAGGCAAGCTGAA 2580
Db 2521 TGGGAGCGTGGGCTGAGCGGCTGTAAGAGGAGAGAGTGAAGAGGCAAGCTGAA 2580
Qy 2581 GCTGCGAAGTGTAGTGTGTTCAAGGAGTGTGAGTTTCCGTGCTTCTGTGAGC 2640
Db 2581 GCTGCGAAGTGTAGTGTGTTCAAGGAGTGTGAGTTTCCGTGCTTCTGTGAGC 2640

Db 2581 GCTGCGAAGTGTAGTGTGTTTCAAGGAGTGTGAGTTTCCGTGCTTCTGTGAGC 2640
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Db 2641 CTTTATATCTTTCTCTGCTTGGAGAGAAAGTCTATTTCAATGAAGAGTGCAGTTTC 2700
Qy 2701 ATTAAGTCAAGCTGTAAATTCAGAGGAGTGTGATGGGTTTCTCTCAAGAGGCTTAT 2760
Db 2701 ATTAAGTCAAGCTGTAAATTCAGAGGAGTGTGATGGGTTTCTCTCAAGAGGCTTAT 2760
Qy 2761 TTAATGGAAATTAAGAAACGAGCTCATTTCTTAGGCGGTTAATTCAGAAAGTGAC 2820
Db 2761 TTAATGGAAATTAAGAAACGAGCTCATTTCTTAGGCGGTTAATTCAGAAAGTGAC 2820
Qy 2821 TGGAGCTTTTCTTTCATGCTCTTGGGCAACTACTAGCCCTGTGTGAGCTTGGCTTA 2880
Db 2821 TGGAGCTTTTCTTTCATGCTCTTGGGCAACTACTAGCCCTGTGTGAGCTTGGCTTA 2880
Qy 2881 TGCAGACGCTGAAATTCGAAATCAGAGACTCGATTTCTTTCTGTGTGCTGCAAT 2940
Db 2881 TGCAGACGCTGAAATTCGAAATCAGAGACTCGATTTCTTTCTGTGTGCTGCAAT 2940
Qy 2941 GGTGGCTGTGAGACCTGTGGGCAAGTCTCTCTTCCCTGGGCAATAGTCTTCTGCT 3000
Db 2941 GGTGGCTGTGAGACCTGTGGGCAAGTCTCTCTTCCCTGGGCAATAGTCTTCTGCT 3000
Qy 3001 ATTAAGACCTTTCAGCTCTGCTGTCTGTGAACATTTCCCTGTGATTTCTGTGAGGG 3060
Db 3001 ATTAAGACCTTTCAGCTCTGCTGTCTGTGTGAACATTTCCCTGTGATTTCTGTGAGGG 3060
Qy 3061 GGATGTTGAGAGGAG 3120
Db 3061 GGATGTTGAGAGGAG 3120
Qy 3121 GAGCAG 3180
Db 3121 GAGCAG 3180
Qy 3181 CAGAGCGAG 3240
Db 3181 CAGAGCGAG 3240
Qy 3241 TCCCTAAGCATTAAGCAATGGCATTTGCCAATTAACCAAAAGATGAGAGAGATGCT 3300
Db 3241 TCCCTAAGCATTAAGCAATGGCATTTGCCAATTAACCAAAAGATGAGAGAGATGCT 3300
Qy 3301 GGATGCTTTTCTGAGATTCAAAACTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3360
Db 3301 GGATGCTTTTCTGAGATTCAAAACTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3360
Qy 3361 TTAATCTTTTCACTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420
Db 3361 TTAATCTTTTCACTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420
Qy 3421 AGTACCTGACAG 3480
Db 3421 AGTACCTGACAG 3480
Qy 3481 AAGATTTCAATTAAG 3540
Db 3481 AAGATTTCAATTAAG 3540
Qy 3541 GTTCTAG 3600
Db 3541 GTTCTAG 3600
Qy 3601 CCGATTTCTAATTAATTAATTTTCTTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 3660
Db 3601 CCGATTTCTAATTAATTAATTTTCTTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3660
Qy 3661 GTAGTAATGAG 3720
Db 3661 GTAGTAATGAG 3720

Db	181	CAGATGTGTCTCTGACAGAAAGCTATTCTTCAGAAAACATACATCCAAATATGTATATC	240
Qy	241	CATCAAAACAGAGCTAAGAAACAGGAATAGATGGGCACTTGCCCAAGAAAAATCCAG	300
Db	241	CATCAAAACAGAGCTAAGAAACAGGAATAGATGGGCACTTGCCCAAGAAAAATCCAG	300
Qy	301	GAGGCGAAATAAGAGAAAATAAAGCTTTTCCCTGGTTTATTTATTCAGAAAAAAG	360
Db	301	GAGGCGAAATAAGAGAAAATAAAGCTTTTCCCTGGTTTATTTATTCAGAAAAAAG	360
Qy	361	ATGAGGACCAAAATCAATGATTAAGAAAAACAGCTCAGAAAAAGATGTTCCAAATTGG	420
Db	361	ATGAGGACCAAAATCAATGATTAAGAAAAACAGCTCAGAAAAAGATGTTCCAAATTGG	420
Qy	421	TAATTAAGTATTTGTTCCTTGGGAGAAAGCTCCATGTGAGCTTGATGGGAAAATGGGA	480
Db	421	TAATTAAGTATTTGTTCCTTGGGAGAAAGCTCCATGTGAGCTTGATGGGAAAATGGGA	480
Qy	481	AAACGTCAAAAGCATGATCTGATCGATGCCAAAGTGATATTATTTAAAAACAGAT	540
Db	481	AAACGTCAAAAGCATGATCTGATCGATGCCAAAGTGATATTATTTAAAAACAGAT	540
Qy	541	GGCATCACTGTGGGAGGCGAAGTTGAGAAAGTCATGTTAGCAAAAGACATAACATAAC	600
Db	541	GGCATCACTGTGGGAGGCGAAGTTGAGAAAGTCATGTTAGCAAAAGACATAACATAAC	600
Qy	601	AGCAAAATCAAAATTTCCGCAAAATGCAAGAGAAAATGGGACCTGGAAAGCTTCTACAC	660
Db	601	AGCAAAATCAAAATTTCCGCAAAATGCAAGAGAAAATGGGACCTGGAAAGCTTCTACAC	660
Qy	661	AGTGAATTAGGCACTTGACCATGTTGGCAACACTTCCCGTCTATACAGGGAAACACAAA	720
Db	661	AGTGAATTAGGCACTTGACCATGTTGGCAACACTTCCCGTCTATACAGGGAAACACAAA	720
Qy	721	ATTGATCGGGCTAAAGCCTTGAATTTCAAGGGAAAATAGAAAACCTAGAGCAAAAACAAA	780
Db	721	ATTGATCGGGCTAAAGCCTTGAATTTCAAGGGAAAATAGAAAACCTAGAGCAAAAACAAA	780
Qy	781	GACATGATTAAGGCAACAGAAACATGTGAGCTTCAAGAGAGAGAGTCCCTCAGCA	840
Db	781	GACATGATTAAGGCAACAGAAACATGTGAGCTTCAAGAGAGAGAGTCCCTCAGCA	840
Qy	841	GGGACCTTGAGGCACTTGCTTTAGGAAAGCCAGTTTCTTAAGGAATCTTAAGAAATC	900
Db	841	GGGACCTTGAGGCACTTGCTTTAGGAAAGCCAGTTTCTTAAGGAATCTTAAGAAATC	900
Qy	901	TTGAAAGATCAAGAAATTTTAACATTTTAAGTATTAAGAAACAAATAGTGAGATGCATATCAG	960
Db	901	TTGAAAGATCAAGAAATTTTAACATTTTAAGTATTAAGAAACAAATAGTGAGATGCATATCAG	960
Qy	961	TTTAAACATGAGTCCCAATTTTAAAGTCAGGATACAAAGATTAACGTGTCCAGCTCC	1020
Db	961	TTTAAACATGAGTCCCAATTTTAAAGTCAGGATACAAAGATTAACGTGTCCAGCTCC	1020
Qy	1021	GGATAGGTCAGAAATCATTTAGAAACAATGTGCTCCCATCTTAACCTTTTCAGAAATGATC	1080
Db	1021	GGATAGGTCAGAAATCATTTAGAAACAATGTGCTCCCATCTTAACCTTTTCAGAAATGATC	1080
Qy	1081	TGTATAGGCTTCACACACAGGCGCAGATGTGTGACCTACAAACCACTCTACACCCCA	1140
Db	1081	TGTATAGGCTTCACACACAGGCGCAGATGTGTGACCTACAAACCACTCTACACCCCA	1140
Qy	1141	GTCCTTCACACATTTGTTAACGTGTATCTCAGTATGCTCCATTAACAAATGCCACCTCCCC	1200
Db	1141	GTCCTTCACACATTTGTTAACGTGTATCTCAGTATGCTCCATTAACAAATGCCACCTCCCC	1200
Qy	1201	TGTGACGCCCACTCCGCGCTCACAGGAAGTCTTCCCACTTAAGACTTGTGATCAAGATGT	1260
Db	1201	TGTGACGCCCACTCCGCGCTCACAGGAAGTCTTCCCACTTAAGACTTGTGATCAAGATGT	1260
Qy	1261	TACAGCCAGAGACTCCGTAGGGGTAGGGTCTGTGTCTTAACACTACCTGTATGCTTAC	1320
Db	1261	TACAGCCAGAGACTCCGTAGGGGTAGGGTCTGTGTCTTAACACTACCTGTATGCTTAC	1320

QY 2401 CCAGAAAGAAATGAGAGGAGAACTAGTCTAAGAGATCTGAGGGAGCAAGTGTTC 2460
Db 2401 CCAGAAAGAAATGAGAGGAGAACTAGTCTAAGAGATCTGAGGGAGCAAGTGTTC 2460
QY 2461 CTCAGAGGAAAGGGGCTTCCAGCTCCAGAGAAATTCAGAGAGTGGGACCTGCAAGGAG 2520
Db 2461 CTCAGAGGAAAGGGGCTTCCAGCTCCAGAGAAATTCAGAGAGTGGGACCTGCAAGGAG 2520
QY 2521 TGGGAGCGCTGGGGCTGAGCGGGGCTGAAAGGAGAGAGTGAAGGAGGAGGAGGAG 2580
Db 2521 TGGGAGCGCTGGGGCTGAGCGGGGCTGAAAGGAGAGAGTGAAGGAGGAGGAGGAG 2580
QY 2581 GCTGCCAGATGTTCACTGTTGTTCAAGGGGCTGGAGATTTTCGTTCTCTGTAAC 2640
Db 2581 GCTGCCAGATGTTCACTGTTGTTCAAGGGGCTGGAGATTTTCGTTCTCTGTAAC 2640
QY 2641 CTTTATCTTTCTCTGCTTGAAGAGAGAGTCTATTCTCAATGAAGGAGTCAAGTTTC 2700
Db 2641 CTTTATCTTTCTCTGCTTGAAGAGAGTCTATTCTCAATGAAGGAGTCAAGTTTC 2700
QY 2701 ATAAAGTCACTGTTAAATTCAGAGGCTGCAAGGATTTCCCTCAGAGAGGCTTTAT 2760
Db 2701 ATAAAGTCACTGTTAAATTCAGAGGCTGCAAGGATTTCCCTCAGAGAGGCTTTAT 2760
QY 2761 TTAATGGGAATATGAGAGGAGAGTCTATTCCTAGGCTTTAATTAACGAGAGAGTAC 2820
Db 2761 TTAATGGGAATATGAGAGGAGAGTCTATTCCTAGGCTTTAATTAACGAGAGAGTAC 2820
QY 2821 TGAGTCTTTCTTCTCATGTTCTTGGGCAACTACTCAGGCTGAGTGGTGGACTTGA 2880
Db 2821 TGAGTCTTTCTTCTCATGTTCTTGGGCAACTACTCAGGCTGAGTGGTGGACTTGA 2880
QY 2881 TGAAGACCGTTCGAAAACCTTGAATCAGAGAGTGGTTCCTTCTGTTCTGTCAT 2940
Db 2881 TGAAGACCGTTCGAAAACCTTGAATCAGAGAGTGGTTCCTTCTGTTCTGTCAT 2940
QY 2941 GGTGGCTGTGCGACCGTGGGCAAGTCTCTCTCCCTGAGGCAATGCTTCTCTGCT 3000
Db 2941 GGTGGCTGTGCGACCGTGGGCAAGTCTCTCTCCCTGAGGCAATGCTTCTCTGCT 3000
QY 3001 ATAAAGACCTTTCAGCTCTCTGTTCTGTAACACTTCCCTGATCTCTGTAAGGAG 3060
Db 3001 ATAAAGACCTTTCAGCTCTCTGTTCTGTAACACTTCCCTGATCTCTGTAAGGAG 3060
QY 3061 GGAATGTTGAGAGGAGAGAGAGAGTCTGAGAGTGAAGCCAGAGGAGAGTGAAGG 3120
Db 3061 GGAATGTTGAGAGGAGAGAGAGAGTCTGAGAGTGAAGCCAGAGGAGAGTGAAGG 3120
QY 3121 GGACAGAGAGGAGAGAGAGTGGTGTCTCATCACTCTCATCTCATCTCATCTCATCTC 3180
Db 3121 GGACAGAGAGGAGAGAGAGTGGTGTCTCATCACTCTCATCTCATCTCATCTCATCTC 3180
QY 3181 CAGAGCCGAGAGCCACATGCTTCAGAGAAAGTCTAATGAACCCACAGCCACATTTTCT 3240
Db 3181 CAGAGCCGAGAGCCACATGCTTCAGAGAAAGTCTAATGAACCCACAGCCACATTTTCT 3240
QY 3241 TCCCTAAGCATAGACATGCTTGGCATTAACCAAAAGAGTGAAGAGTGAAGTGAAGT 3300
Db 3241 TCCCTAAGCATAGACATGCTTGGCATTAACCAAAAGAGTGAAGAGTGAAGTGAAGT 3300
QY 3301 GGTAGCTTTTCTGCTGCAATTCAAAACCTGGCCAGAGCAAGTGAAGATTCAGAGATTG 3360
Db 3301 GGTAGCTTTTCTGCTGCAATTCAAAACCTGGCCAGAGCAAGTGAAGATTCAGAGATTG 3360
QY 3361 TTAAGCTTTTACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420
Db 3361 TTAAGCTTTTACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420
QY 3421 AGTGAAGTGAAG 3480
Db 3421 AGTGAAGTGAAG 3480
QY 3481 ACAAGTATTCAG 3540

Db 3481 ACAAGTATTCAG 3540
QY 3541 GTTCTGAG 3600
Db 3541 GTTCTGAG 3600
QY 3601 CCGATTTCTAATCTAATATTTTCTTACAGCTGAGTAAATTCAGAGAGTCAAG 3660
Db 3601 CCGATTTCTAATCTAATATTTTCTTACAGCTGAGTAAATTCAGAGAGTCAAG 3660
QY 3661 GTAGTAATCTAGGCTTAAGATTTACTAATTTCTCTTAATGAAGTCTTTCTGCTGT 3720
Db 3661 GTAGTAATCTAGGCTTAAGATTTACTAATTTCTCTTAATGAAGTCTTTCTGCTGT 3720
QY 3721 GGAATTGAG 3780
Db 3721 GGAATTGAG 3780
QY 3781 TAAAGCCAAACAGATTCAGAGCTGAGTCTTCTGAGTATGATTTGTTGAAGAT 3840
Db 3781 TAAAGCCAAACAGATTCAGAGCTGAGTCTTCTGAGTATGATTTGTTGAAGAT 3840
QY 3841 CATTTGAGAGAGTGTACTATCTGATTCAGAAATGAGAGTGAAGTCTTCTGAGCTG 3900
Db 3841 CATTTGAGAGAGTGTACTATCTGATTCAGAAATGAGAGTGAAGTCTTCTGAGCTG 3900
QY 3901 TAAACAAACAGAGTGTAAATGTTCAAGTTCAGGCTTAACTGAGAGAGAGAGAGAG 3959
Db 3901 TAAACAAACAGAGTGTAAATGTTCAAGTTCAGGCTTAACTGAGAGAGAGAGAGAG 3960
QY 3960 AAGATGATCTTTGAG 4019
Db 3961 AAGATGATCTTTGAG 4019
QY 4020 CAGTTGGAATATTTACTTACAGAGATTCAGAGTGTGTTGATTAACAGAGAGAG 4079
Db 4020 CAGTTGGAATATTTACTTACAGAGATTCAGAGTGTGTTGATTAACAGAGAGAG 4079
QY 4080 TTGCTCAAAGAGATCTAATTTCAAGTGTCTTAAAGTACTTCTGAGAGTGTGTATA 4139
Db 4080 TTGCTCAAAGAGATCTAATTTCAAGTGTCTTAAAGTACTTCTGAGAGTGTGTATA 4139
QY 4140 TTAATGCTAATGAGAGATTTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4199
Db 4140 TTAATGCTAATGAGAGATTTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4199
QY 4200 GGAATTAATTAACCTAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4259
Db 4200 GGAATTAATTAACCTAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4259
QY 4260 TTGTTTACCACTTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4319
Db 4260 TTGTTTACCACTTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4319
QY 4320 ACTCAAGAGTGAATTAACAGTACCTGATTTTGTATTAACAGAGAGAGAGAGAGAG 4379
Db 4320 ACTCAAGAGTGAATTAACAGTACCTGATTTTGTATTAACAGAGAGAGAGAGAGAG 4379
QY 4380 TTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4439
Db 4380 TTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4439
QY 4440 ACTTGAATTAAG 4499
Db 4440 ACTTGAATTAAG 4499
QY 4500 AATTTGAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4559
Db 4500 AATTTGAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4559
QY 4560 TATATTTGAG 4619


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QY 4210 ACCTACAGTCCAGAAAGCTGTGATTTGAATGAGGAAAAATTACATTTTGTGTTTAC 4269
Db 779 ACCTACAGTCCAGAAAGCTGTGATTTGAATGAGGAAAAATTACATTTTGTGTTTAC 838
QY 4270 CACCTTCTAACTAAATTTAACTTTTATTCATTCGCAATGAGCATAAAGTCAAGTG 4329
Db 839 CACCTTCTAACTAAATTTAACTTTTATTCATTCGCAATGAGCATAAAGTCAAGTG 898
QY 4330 GATAAACAAGACCTGATTTGTTGCTATTCACATGAAATCAACACATTTTATACAT 4389
Db 899 GATAAACAAGACCTGATTTGTTGCTATTCACATGAAATCAACACATTTTATACAT 958
QY 4390 ATTACAGTGTGAGATGAGTGTGATGTAAGTAAATTTTATTCACAAACTACTTTGAAAT 4449
Db 959 ATTACAGTGTGAGATGAGTGTGATGTAAGTAAATTTTATTCACAAACTACTTTGAAAT 1018
QY 4450 TAGACCTGCTGCTGAGATCTGTTTAACTATTTAAATAAACATGTTTAAATTTTGATA 4509
Db 1019 TAGACCTGCTGCTGAGATCTGTTTAACTATTTAAATAAACATGTTTAAATTTTGATA 1078
QY 4510 TTTTGATATATCATATTTTCAATTCATTTGTTTCTTTGTAATCTATATTTTATATTTTG 4569
Db 1079 TTTTGATATATCATATTTTCAATTCATTTGTTTCTTTGTAATCTATATTTTATATTTTG 1138
QY 4570 AAAACATCTTTCTGAGAGAGTTCCCGAGATTTCCACCATGAGGTTCTTGGAATGACAC 4629
Db 1139 AAAACATCTTTCTGAGAGAGTTCCCGAGATTTCCACCATGAGGTTCTTGGAATGACAC 1198
QY 4630 ACACAGAGTAAAGCTATTTAGAGGCTAACATTCATTCATTCGCTGCTGAGATGCAAGAT 4689
Db 1199 ACACAGAGTAAAGCTATTTAGAGGCTAACATTCATTCATTCGCTGCTGAGATGCAAGAT 1258
QY 4690 GAAATTTAGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAGAGGCTGAGAGGAGAA 4749
Db 1259 GAAATTTAGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAGAGGCTGAGAGGAGAA 1318
QY 4750 ATCTGCGGCTTCTATAGGAATGCTCTCCCTGAGAGCTGATAGGCTGCTGCTGCTGCTG 4809
Db 1319 ATCTGCGGCTTCTATAGGAATGCTCTCCCTGAGAGCTGATAGGCTGCTGCTGCTGCTG 1378
QY 4810 TGCGTGGCTGTTATTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4869
Db 1379 TGCGTGGCTGTTATTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1438
QY 4870 GTTCTTAAGCATAGTGCCTGCGACAGTGCAGGTTCTCAATGATGTTTCCAGATGAA 4929
Db 1439 GTTCTTAAGCATAGTGCCTGCGACAGTGCAGGTTCTCAATGATGTTTCCAGATGAA 1498
QY 4930 AATATAACTAGAAATATATCTGTTGAATTCAGACACACAGATGCTGCTGCTGCTGCTG 4989
Db 1499 AATATAACTAGAAATATATCTGTTGAATTCAGACACACAGATGCTGCTGCTGCTGCTG 1558
QY 4990 GTGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5049
Db 1559 GTGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1618
QY 5050 TTATTTGGGCTATGGGCTGATTAATTTGGGATGTTCTTTTAAAGAAATCCCAAGAGAC 5109
Db 1619 TTATTTGGGCTATGGGCTGATTAATTTGGGATGTTCTTTTAAAGAAATCCCAAGAGAC 1678
QY 5110 TTCTGGAAGCTTATTTTCTAAGATCTTGCTGAGAGGCTGAGAGCAACCCCTGTGAC 5169
Db 1679 TTCTGGAAGCTTATTTTCTAAGATCTTGCTGAGAGGCTGAGAGCAACCCCTGTGAC 1738
QY 5170 AGCCCCACCCAGCTCAGCTGAGCACTCTGTCTTCCCTCATGAGAGGCTGAGCTCCCGAG 5229
Db 1739 AGCCCCACCCAGCTCAGCTGAGCACTCTGTCTTCCCTCATGAGAGGCTGAGCTCCCGAG 1798
QY 5230 TATATATAAAGCTCTGAGAGCTGAGGCTGAGAGCAAGG 5271
Db 1799 TATATATAAAGCTCTGAGAGCTGAGGCTGAGAGCAAGG 1840

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RESULT 9
US-09-306-828-38
; Sequence 38, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 38
; LENGTH: 227
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-38

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Query Match 4.3%; Score 227; DB 4; Length 283;
Best Local Similarity 100.0%; Pred.No.3.8e-47;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5045 AACTATATATGGGATATGGGATGATTAATTTGGGATGTTCTTTTAAAGAAATCCCAA 5104
Db 1 AACTATATATGGGATATGGGATGATTAATTTGGGATGTTCTTTTAAAGAAATCCCAA 60
QY 5105 CAGCTTCTGGAAGCTTATTTTCTAAGATCTTGTCTGAGAGCTGAGGCAACCCCTG 5164
Db 61 CAGCTTCTGGAAGCTTATTTTCTAAGATCTTGTCTGAGAGCTGAGGCAACCCCTG 120
QY 5165 TGACACAGCCCAACCCAGCTCAGTGGGCACTCTCTTCCCAATGAGGCTGCTG 5224
Db 121 TGACACAGCCCAACCCAGCTCAGTGGGCACTCTCTTCCCAATGAGGCTGCTG 180
QY 5225 CCGATATATATTAACCTCTCTGAGAGCTGGGATGAGCAGCAGAGG 5271
Db 181 CCGATATATATTAACCTCTCTGAGAGCTGGGATGAGCAGCAGAGG 227

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RESULT 10
US-09-306-828-37
; Sequence 37, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 37
; LENGTH: 283
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-37

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Query Match 4.3%; Score 227; DB 4; Length 283;
Best Local Similarity 100.0%; Pred.No.3.8e-47;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5045 AACTATATATGGGATATGGGATGATTAATTTGGGATGTTCTTTTAAAGAAATCCCAA 5104
Db 1 AACTATATATGGGATATGGGATGATTAATTTGGGATGTTCTTTTAAAGAAATCCCAA 60

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QY 5105 CAGACTTCTGSAAGGTTATTTCTAGAACTTGTGCGGAGGCGAAGCAACCCCTG 5164
DB 61 CAGACTTCTGSAAGGTTATTTCTAGAACTTGTGCGGAGGCGAAGCAACCCCTG 120
QY 5165 TGCACAGCCCGCCAGCCTCAAGTGGCCAGCTGTCTTCCCGCATGAAGGCTGAGCTC 5224
DB 121 TGCACAGCCCGCCAGCCTCAAGTGGCCAGCTGTCTTCCCGCATGAAGGCTGAGCTC 180
QY 5225 CCAGATATATTAACCTCTGAGAGCTGCGGCATGAGCGCAGAG 5271
DB 181 CCAGATATATTAACCTCTGAGAGCTGCGGCATGAGCGCAGAG 227

RESULT 11

US-09-813-817-3/c
Sequence 3, Application US/09813817
Patent No. 634583
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CL001178
CURRENT APPLICATION NUMBER: US/09/813,817
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 59065
TYPE: DNA
ORGANISM: Human
US-09-813-817-3

Query Match 3.4%; Score 177.6; DB 4; Length 59065;
Best Local Similarity 77.5%; Pred. No. 1.4e-33;
Matches 231; Conservative 0; Mismatches 59; Indels 8; Gaps 1;

QY 1277 GTGAGGCTGAGGCTGTCTGTCTTACACCTGATGCTTACACCTGAGCTACTGCA 1336
DB 2380 GTGAGGCTGTCTGTCTGTCTTACACCTGATGCTGAGCTGCTGCTACTGCA 23741
QY 1337 ACCTGCTGCTCCAGGTTCAAGCAATTCCTGTCTGAGCTCCCGGCTAGCTGGACTA 1396
DB 23740 ACCTGCTGCTCCAGGTTCAAGCAATTCCTGTCTGAGCTCCCGGCTAGCTGGACTA 23681
QY 1397 CAGGCGCAGCC-----CGGCTAATTTTGTGATTTGTGATGAGATGGGGTTTCAAC 1448
DB 23680 CAGGCGCAGCCAGCCAGCTGCTGCTAATTTTGTGATTTGTGATGAGATGGGGTTTCAAC 23621
QY 1449 ATATTAGCCCGGCTGCTTGAACCTGACCTGAGTGATGACCCCACTCAGCTCCT 1508
DB 23620 ATATTAGCTGAGCTGTCTTGAACCTGACCTGAGTGATGACCTGCTCAGCTCCTC 23561
QY 1509 AAAGTCTGAGATTACAGCATGAGTACCGCGCCGCGCAGGCTGAGTTTAATA 1566
DB 23560 AAAGTCTGAGATTACAGCATGAGTACCGCGCCGCGCAGGCTGAGTTTAATA 23503

RESULT 12

US-09-978-197-3/c
Sequence 3, Application US/09978197
Patent No. 6403353
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CL001178DIV
CURRENT APPLICATION NUMBER: US/09/978,197
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/813,817
PRIOR FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 59065
TYPE: DNA
ORGANISM: Human
US-09-978-197-3

Query Match 3.4%; Score 177.6; DB 4; Length 59065;
Best Local Similarity 77.5%; Pred. No. 1.4e-33;
Matches 231; Conservative 0; Mismatches 59; Indels 8; Gaps 1;

QY 1277 GTGAGGCTGAGGCTGTCTGTCTTACACCTGATGCTTACACCTGAGCTACTGCA 1336
DB 2380 GTGAGGCTGTCTGTCTGTCTTACACCTGATGCTGAGCTGCTGCTACTGCA 23741
QY 1337 ACCTGCTGCTCCAGGTTCAAGCAATTCCTGTCTGAGCTCCCGGCTAGCTGGACTA 1396
DB 23740 ACCTGCTGCTCCAGGTTCAAGCAATTCCTGTCTGAGCTCCCGGCTAGCTGGACTA 23681
QY 1397 CAGGCGCAGCC-----CGGCTAATTTTGTGATTTGTGATGAGATGGGGTTTCAAC 1448
DB 23680 CAGGCGCAGCCAGCCAGCTGCTGCTAATTTTGTGATTTGTGATGAGATGGGGTTTCAAC 23621
QY 1449 ATATTAGCCCGGCTGCTTGAACCTGACCTGAGTGATGACCCCACTCAGCTCCT 1508
DB 23620 ATATTAGCTGAGCTGTCTTGAACCTGACCTGAGTGATGACCTGCTCAGCTCCTC 23561
QY 1509 AAAGTCTGAGATTACAGCATGAGTACCGCGCCGCGCAGGCTGAGTTTAATA 1566
DB 23560 AAAGTCTGAGATTACAGCATGAGTACCGCGCCGCGCAGGCTGAGTTTAATA 23503

RESULT 13

US-09-495-050A-138
Sequence 138, Application US/09495050A
Patent No. 6492505
GENERAL INFORMATION:
APPLICANT: Roopa, Reddy
APPLICANT: Guejler, Karl, J.
APPLICANT: Au-Yang, Janice
TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
FILE REFERENCE: PA-0013 US
CURRENT APPLICATION NUMBER: US/09/495,050A
CURRENT FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/118,318
PRIOR FILING DATE: February 1, 1999
NUMBER OF SEQ ID NOS: 305
SOFTWARE: PERL Program
SEQ ID NO 138
LENGTH: 851
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. 6492505 1516908B1
US-09-495-050A-138

Query Match 3.4%; Score 176.8; DB 4; Length 851;
Best Local Similarity 87.4%; Pred. No. 2.4e-34;
Matches 208; Conservative 0; Mismatches 22; Indels 8; Gaps 1;

QY 1321 ACCTGAGCTCAGTGAACCTTGTGCTCCAGGTTCAAGCAATTCCTGTCTGAGCTCCTC 1380
DB 170 ATCTCAGCTCAGTGAACCTTGTGCTCCAGGTTCAAGCAATTCCTGTCTGAGCTCCTC 229
QY 1381 CGGCTAGCTGGAGTCAAGGCG-----CAGGCGGCTAATTTTGTGATGTTAGTA 1432
DB 230 CGGCTAGCTGGAGTCAAGGCGGCTGCGCCCAAGCCGCGTAATTTTGTGATGTTAGTA 289
QY 1433 GAGATGGGTTTCAACATTAATGACCGGCTGCTGCTTGAATCTGACCTGAGTGATCA 1492
DB 290 GAAATGGGTTTCAACCTTGTGCTGAGCTTGTCTCAAACTCTGACCTGAGTGATCA 349

PRIOR APPLICATION NUMBER:	US 60/145,915
PRIOR FILING DATE:	1999-07-27
PRIOR APPLICATION NUMBER:	US 60/146,453
PRIOR FILING DATE:	1999-07-29
PRIOR APPLICATION NUMBER:	US 60/146,452
PRIOR FILING DATE:	1999-07-29
PRIOR APPLICATION NUMBER:	US 60/162,288
PRIOR FILING DATE:	1999-10-28
PRIOR APPLICATION NUMBER:	US 09/146,384
PRIOR FILING DATE:	1999-10-12
NUMBER OF SEQ ID NOS:	231
SOFTWARE:	Patent.pm
SEQ ID NO 37	
LENGTH:	1154
TYPE:	DNA
ORGANISM:	Homo sapiens
FEATURE:	
NAME/KEY:	5'UTR
LOCATION:	1..719
FEATURE:	
NAME/KEY:	CDS
LOCATION:	720..1118
FEATURE:	
NAME/KEY:	3'UTR
LOCATION:	1119..1154
FEATURE:	
NAME/KEY:	polya.signal
LOCATION:	1131..1136
FEATURE:	
NAME/KEY:	allele
LOCATION:	131
OTHER INFORMATION:	8-121-187 : polymorphic base A or C
FEATURE:	
NAME/KEY:	allele
LOCATION:	313
OTHER INFORMATION:	8-122-271 : deletion of CAA
FEATURE:	
NAME/KEY:	allele
LOCATION:	141
OTHER INFORMATION:	8-122-272 : polymorphic base A or G
FEATURE:	
NAME/KEY:	allele
LOCATION:	368
OTHER INFORMATION:	8-122-326 : polymorphic base A or C
FEATURE:	
NAME/KEY:	allele
LOCATION:	390
OTHER INFORMATION:	8-123-55 : polymorphic base A or T
FEATURE:	
NAME/KEY:	allele
LOCATION:	814
OTHER INFORMATION:	8-128-61 : polymorphic base G or C
FEATURE:	
NAME/KEY:	allele
LOCATION:	821
OTHER INFORMATION:	8-128-68 : polymorphic base C or T
FEATURE:	
NAME/KEY:	allele
LOCATION:	822
OTHER INFORMATION:	8-128-69 : polymorphic base A or G
FEATURE:	
NAME/KEY:	allele
LOCATION:	838
OTHER INFORMATION:	8-128-85 : polymorphic base A or C
FEATURE:	
NAME/KEY:	allele
LOCATION:	897
OTHER INFORMATION:	8-129-50 : polymorphic base C or T
FEATURE:	
NAME/KEY:	allele
LOCATION:	908
OTHER INFORMATION:	8-129-60 : deletion of A
US-09-539-333D-37	

Query Match 3.4%; Score 176.6; DB 4; Length 1154;
Best Local Similarity 75.9%; Pred. No. 3.2e-34;
Matches 233; Conservative 1; Mismatches 65; Indels 8; Gaps 1;

QY	1253	CACGATGTTACAGCCAGAAAGCTCCGAGAGGTGAGGCTCTGTCTTACACTTACTGTA	1312
DB	820	CAGCAGSCTCCAGAGTTAATTGAGATGAGTCTCACTCTGTTGCCAGGCTGAGTGCA	761
QY	1313	TGCTTACACCTGAGCTCACTGCAACCTCTGCTCCAGGTTCAAGCAATTCTCTGCT	1372
DB	760	GTGATGATCTTGAGCTCACTGCAACCTCGGCTCCAGGTTCAAGCAATTCTCTGCT	701
QY	1373	CAGCTTCCCGCTAGCTGGGACTACAGC-----GACGCCCGGCTAATTTTGTAT	1424
DB	700	CAGCTTCCCGAGTAGCTGGGACTACAGCAGCTGCCACCATGCTGGCTAATTTTGTAT	641
QY	1425	TGTTAGTAGAGATGGGTTTACCATATTAGCCCGGCTGCTTGAATCTCCAGCTCAG	1484
DB	640	TTTTAGTAGAGATGGGTTTACCATATTGCTCAGGCTGCTTGAATCTCCAGCTCAG	581
QY	1485	GTGATCACCACCTCAGCTCTTAAAGTGTGGGATTACAGGCATGAGTACCCGCGCC	1544
DB	580	GTGATCTGCCCGCTCGGCTCCCAAGTGTGGGATTACAGGTGTAGCCACTGAGGCT	521
QY	1545	GGCCAAG 1551	
DB	520	GGCCAAG 514	

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Job time : 343 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 18, 2004, 19:21:17; Search time 1873 Seconds
(without alignments)
11955.287 Million cell updates/sec

Title: US-09-227-881-34

Perfect score: 5271
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Scoring table: IDENTITY NUC
Gapop 10-0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1380s:*
3: geneseqn1990s:*
4: geneseqn2000s:*
5: geneseqn2001s:*
6: geneseqn2001bs:*
7: geneseqn2002s:*
8: geneseqn2003as:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5271	100.0	6169	2	AAV51368 Human TIG
2	5271	100.0	6169	3	AAAS7486 A TIGR (t
3	5269.4	100.0	5271	3	AAAS7511 A TIGR (t
4	5246.4	99.5	5299	2	AAV51361
5	5246.4	99.5	5300	2	AAAS7484
6	5246.4	99.5	5300	2	AAV51365
7	5244.8	99.5	5300	2	AAV51367
8	5244.8	99.5	5300	2	AAV51363
9	5244.8	99.5	5300	2	AAV51366
10	5244.8	99.5	5300	2	AAV51362
11	5232.4	99.3	5304	2	AAV51364
12	5224.4	99.1	5304	2	AAAS7485
13	1804.4	34.2	2800	6	AAZ37968 Human GLC
14	394.4	7.5	476	6	ABA96249 Human GLC
15	394.4	7.5	1086	7	ACA64937 Human GLC
16	227	4.3	227	3	AAAS7515
17	227	4.3	283	3	AAAS7514
18	185.8	3.5	2847	4	AAK82073 Human imm
19	185.8	3.5	2847	5	ABAI8224 Human cdn
20	184.4	3.5	1744	6	AOB63691 Human ner
21	183.2	3.5	41936	6	AB167924 Ovary can
22	182.2	3.5	5367	5	AAAS80633 DNA encod
23	181	3.4	8017	4	AAK70627 Human imm

C	24	181	3.4	8017	5	ABAI9015	ABAI9015 Human ner
C	25	181	3.4	19798	9	ADD71026	ADD71026 Human nch
C	26	180.6	3.4	10483	4	AAK80686	AAK80686 Human imm
C	27	180.6	3.4	39729	9	ADCC86832	ADCC86832 Human GPC
C	28	180.6	3.4	54108	6	ABK22782	ABK22782 Human hig
C	29	180.6	3.4	57273	5	ABK22784	ABK22784 Human hig
C	30	180.6	3.4	66933	5	ABK22784	ABK22784 Human hig
C	31	180.6	3.4	66933	7	ACC45366	ACC45366 Human HBM
C	32	180.6	3.4	66933	9	ADB98066	ADB98066 HBM-relat
C	33	180.6	3.4	66933	9	ADB98066	ADB98066 HBM-relat
C	34	180.6	3.4	72049	5	ADB82623	ADB82623 Human HBM
C	35	180.6	3.4	72049	9	ADB98064	ADB98064 HBM-relat
C	36	180.6	3.4	72049	9	ADB82623	ADB82623 Human HBM
C	37	180.6	3.4	3015	4	AAK85238	AAK85238 Human imm
C	38	179.8	3.4	1325	5	ABAI8925	ABAI8925 Human ner
C	39	179.8	3.4	100301	6	ABQ88176	ABQ88176 Human ost
C	40	179.8	3.4	2233	7	AAK77256	AAK77256 Human imm
C	41	179.6	3.4	6487	7	ABE67966	ABE67966 Human sec
C	42	179.4	3.4	6487	7	ABE74409	ABE74409 Secreted
C	43	179.4	3.4	6487	7	ADA98861	ADA98861 Human sec
C	44	179.4	3.4	6487	7	ADA44475	ADA44475 Human sec
C	45	179.4	3.4	6487	7	ADA44475	ADA44475 Human sec

ALIGNMENTS

RESULT 1	AAV51368	standard; DNA; 6169 BP.
ID	AAV51368	
XX	AAV51368	
AC	AAV51368	
XX	27-OCT-1998	(first entry)
DT	27-OCT-1998	
XX	Human TIGR upstream region and exon 1 DNA.	
DE	Human TIGR upstream region and exon 1 DNA.	
XX	TIGR; trabecular meshwork induced glucocorticoid response protein; human;	
KW	diagnosis; glaucoma; polymorphism; steroid sensitivity; ss.	
KW	diagnosis; glaucoma; polymorphism; steroid sensitivity; ss.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	Key	Location/Qualifiers
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PS Claim 37; Fig 3; 105bp; English.

CC This sequence is a trabecular meshwork induced glucocorticoid response
CC protein (TIGR) upstream region and exon 1. This DNA sequence can be used
CC in a method for diagnosing glaucoma in a patient. The method involves the
CC detection of polymorphisms whose presence is predictive of a mutation
CC affecting TIGR response in the patient and can be diagnostic of glaucoma
CC or steroid sensitivity. Base substitutions and base additions upstream of
CC and within TIGR exons can also be used to diagnose glaucoma
XX

SQ Sequence 6169 BP; 1702 A; 1389 C; 1491 G; 1587 T; 0 U; 0 Other;

Query Match 100.0%; Score 5271; DB 2; Length 6169;

Best Local Similarity 100.0%; Pred. No. 0; Matches 5271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATCTTTGTCAGTTTACTCAGGGCTATATGAAATGAAATAGTAAACCAATGGAAG 60
QY 61 TCCATTAACCTGTATAGCTCCATTGCGATGTATGCTTTGGCAGATGATTAAGATCA 120
DB 61 TCCATTAACCTGTATAGCTCCATTGCGATGTATGCTTTGGCAGATGATTAAGATCA 120
QY 121 GGAAGAAGAGATATCCAGCTTAGCCAGTGTCCAGGCTGTCTGCTCTTATTTAGTGA 180
DB 121 GGAAGAAGAGATATCCAGCTTAGCCAGTGTCCAGGCTGTCTGCTCTTATTTAGTGA 180
QY 181 CAGATGTCTCTCTGACAGAACTATTTCTTCAGAAACATCAATCCAAATGCTAATC 240
DB 181 CAGATGTCTCTCTGACAGAACTATTTCTTCAGAAACATCAATCCAAATGCTAATC 240
QY 241 CATCAAAACGAGCTTAAGAAACAGAAATGAGATGAGGCTTCCCGAAGAAATGCGCAG 300
DB 241 CATCAAAACGAGCTTAAGAAACAGAAATGAGATGAGGCTTCCCGAAGAAATGCGCAG 300
QY 301 GAGAGCAAAATATGATGAAATAAATCTTCCCTTTGTTTAAATTCAGAAATAATG 360
DB 301 GAGAGCAAAATATGATGAAATAAATCTTCCCTTTGTTTAAATTCAGAAATAATG 360
QY 361 ATGAGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
DB 361 ATGAGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 421 TAATTAAGATTTTCTCTGGAAGAGAGCTCCATGAGCTGATGAGGAAATGAGGA 480
DB 421 TAATTAAGATTTTCTCTGGAAGAGAGCTCCATGAGCTGATGAGGAAATGAGGA 480
QY 481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAGTGGATTATTTAAAAACGAT 540
DB 481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAGTGGATTATTTAAAAACGAT 540
QY 541 GGCATCACTCTGGGAGGAGGAGTTCAGGAAGGTGATGTTAGCAAAAGCATTAATAC 600
DB 541 GGCATCACTCTGGGAGGAGGAGTTCAGGAAGGTGATGTTAGCAAAAGCATTAATAC 600
QY 601 AGCAAAATCAAAATTCGCAATGAGAGGAAATGAGGAGGAGGAGGAGGAGGAGGAG 660
DB 601 AGCAAAATCAAAATTCGCAATGAGAGGAAATGAGGAGGAGGAGGAGGAGGAGGAG 660
QY 661 AGTATTAAGGAGTTCAGGATGATGATGATGATGATGATGATGATGATGATGATG 720
DB 661 AGTATTAAGGAGTTCAGGATGATGATGATGATGATGATGATGATGATGATGATG 720
QY 721 ATTGATGGGCTAAGCTGAGCTTCAAGGAAATATGAAATCTGAGGAGGAGGAGGAG 780
DB 721 ATTGATGGGCTAAGCTGAGCTTCAAGGAAATATGAAATCTGAGGAGGAGGAGGAG 780
QY 781 GACATGTTTAAAGGCAACCAATTTGAGCTTCAAGGAGGAGGAGGAGGAGGAGGAGG 840
DB 781 GACATGTTTAAAGGCAACCAATTTGAGCTTCAAGGAGGAGGAGGAGGAGGAGGAGG 840
QY 841 GGAACCTGAGGATTTGCTTTAGGAAGGCAAGTTTCTTAAGAAATCTTAAGAACTC 900
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DB 841 GGAACCTGAGGATTTGCTTTAGGAAGGCAAGTTTCTTAAGAAATCTTAAGAACTC 900
QY 901 TTGAAGATCATGAAATTTTAAACATTTTAAATGATTAAGAAATGAGATGATTAACAG 960
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DB 961 TTGAAGATCATGAAATTTTAAACATTTTAAATGATTAAGAAATGAGATGATTAACAG 1020
QY 1021 GATAGGTCAGAAATCATTAAGAAATCACTGTCCTCATCTTAATCTTTTCAAGATGATC 1080
DB 1021 GATAGGTCAGAAATCATTAAGAAATCACTGTCCTCATCTTAATCTTTTCAAGATGATC 1080
QY 1081 TGTCAATGCTTCAACACAGAGGCGGATGATGATGATGATGATGATGATGATGATGAT 1140
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QY	4501	ATTTGATATTGTGAAATTCATATTTCATTTCAATTGTTCTTTGATCTAATTTT	4560
Db	4501	ATTTGATATTGTGAAATTCATATTTCATTTCAATTGTTCTTTGATCTAATTTT	4560
QY	4561	ATATTTTGAAGAAACATCTTCTGAGAAAGTTCGCCAGATTTCACCAATGAGTCTTG	4620
Db	4561	ATATATTTGAAGAAACATCTTCTGAGAAAGTTCGCCAGATTTCACCAATGAGTCTTG	4620
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Db	4621	CATGCACACACAGAGTAAAGATCGATTGAGAGCTTAACTTGACATTTGGTGCCTAGA	4680
QY	4681	TGCAAGACTGAAATTTGAAAGTTCTCCCAAGATPACAGTTGTTTAAAGCTAAGGGTG	4740
Db	4681	TGCAAGACTGAAATTTGAAAGTTCTCCCAAGATPACAGTTGTTTAAAGCTAAGGGTG	4740
QY	4741	AGGGGGGAAATCTGCGCTCTATAGGAATCTCTCCCTGGAAGCTGTAGGGTGCTG	4800
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QY	4801	CTTGTTCTTGCGCTGCTGTAATTTTCTGTGCTCTGCTACGTCCTTAAAGACTTGTT	4860
Db	4801	CTTGTTCTTGCGCTGCTGTAATTTTCTGTGCTCTGCTACGTCCTTAAAGACTTGTT	4860
QY	4861	GGATCTCCAGTCTTAGCATATGATGTCGCGACAGTGAAGTTCATGAGTGTGAGAG	4920
Db	4861	GGATCTCCAGTCTTAGCATATGATGTCGCGACAGTGAAGTTCATGAGTGTGAGAG	4920
QY	4921	TGAATGGAATATTAACATAGAAATATACTGTTGTAATCAGACACACAGTAGTCTG	4980
Db	4921	TGAATGGAATATTAACATAGAAATATACTGTTGTAATCAGACACACAGTAGTCTG	4980
QY	4981	TGTAAGTGTGTATCGT	5040
Db	4981	TGTAAGTGTGTATCGT	5040
QY	5041	TAGGAACCTATTATGCGGATAGGTCATATAATGGGATTTCTTTTAAAAAGAACTC	5100
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Db	5101	CAAAACAGACTTCTGGAAGGTTATTTTCTAAGATCTTGTGCGAGGCTAAGCAACCC	5160
QY	5161	CTGTGTGACAGCCCAACCCAGCTCAGTGTGCGACACCTCTGTCTTCCCAATGAAGGCTG	5220
Db	5161	CTGTGTGACAGCCCAACCCAGCTCAGTGTGCGACACCTCTGTCTTCCCAATGAAGGCTG	5220
QY	5221	GCTCCCAATATATTAACCTCTTGGAAGCTGCGCATGAGCCAGCAAGG	5271

Db 5221 GCTCCCAAGTATATTAACCTCTGTGAGCTGGAGCATGAGCCACAAGG 5271

RESULT 2
ID AAA57486
AAA57486 standard; DNA; 6169 BP.
AC AAA57486;
DT 20-OCT-2000 (first entry)
XX A TIGR (trabecular meshwork inducible glucocorticoid receptor) promoter.
XX KW TIGR; trabecular meshwork inducible glucocorticoid receptor; promoter;
KM glaucoma; steroid sensitivity; progressive ocular hypertension;
KW vision loss; ss.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT mutation replace(4256, G)
FT /*tag= d
FT /*note= "TIGRmt4 mutant"
FT mutation replace(4337, G)
FT /*tag= a
FT /*note= "TIGRmt1 mutant"
FT mutation replace(4950, T)
FT /*tag= b
FT /*note= "TIGRmt2 mutant"
FT mutation 4998
FT /*tag= c
FT /*note= "GTGT added to produce TIGRmt3 mutant"
FT mutation replace(5113, C)
FT /*tag= e
FT /*note= "TIGRmt11 mutant"
PN MO200042220-A1.
PD 20-JUL-2000.
PX
PF 11-JAN-2000; 2000MC-US000559.
PR XX
PR 11-JAN-1999; 99US-00227881.
PR 07-MAY-1999; 99US-00306882.
FA (REGC) UNIV CALIFORNIA.
PI Nguyen TD, Polansky JR, Chen P, Chen H;
DR WPI; 2000-491060/43.
XX
XX
PT Diagnosis, prognosis and treatment of glaucoma, based on detecting
PT specific polymorphisms in the promoter of the trabecular meshwork
PT inducible glucocorticoid receptor gene.
PS Claim 37; Page 105-107; 122pp; English.

The present sequence represents a TIGR (trabecular meshwork inducible glucocorticoid receptor) promoter. The specification describes a method for the diagnosis, prognosis and treatment of glaucoma, based on detecting specific polymorphisms in the promoter of the TIGR gene. The method is used for diagnosis and prognosis of glaucoma (of all types), steroid sensitivity and progressive ocular hypertension that leads to loss of vision. Glaucoma can be treated by administering an agent that binds to cis-acting elements within the TIGR promoter. The TIGR promoter (or other regulatory regions) can be used to express homologous or heterologous genes, particularly for tissue-specific expression of therapeutic transgenes for treating glaucoma, also to generate transgenic animals and in screening for compounds (specific modulators) with diagnostic or therapeutic potential. Fragments of the TIGR sequence can be used as amplification primers or probes, e.g. for isolating related sequences in non-human animals

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XX	Sequence 6169 BP; 1702 A; 1389 C; 1491 G; 1587 T; 0 U; 0 Other;	
SQ	Query Match 100.0%; Score 5271; DB 3; Length 6169;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 5271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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DB	1 ATCTTTGTCAGTTTACCTCAGGCTATTAAGAATGAATGATTAACCAATGTGAAG 60	
QY	61 TCCATTAACCTGTAAGCTCCATTCGATGTAATGCTTTGGAGAGATGATAAATCA 120	
DB	61 TCCATTAACCTGTAAGCTCCATTCGATGTAATGCTTTGGAGAGATGATAAATCA 120	
QY	121 GGAAAGAGAGATATCCAGCTTACGCAAGTGTCCAGGCTGTCTCTTTATTTAGTGA 180	
DB	121 GGAAAGAGAGATATCCAGCTTACGCAAGTGTCCAGGCTGTCTCTTTATTTAGTGA 180	
QY	181 CAGATGTCTCTCCGACGAGAGATCTTCTCAGAAACATCAATCAATATGTAATC 240	
DB	181 CAGATGTCTCTCCGACGAGAGATCTTCTCAGAAACATCAATCAATATGTAATC 240	
QY	241 CATCAACAGAGAGCTAAGAAACAGGAATGAGATGCGCACTTGCCCAAGAAATGCGAG 300	
DB	241 CATCAACAGAGAGCTAAGAAACAGGAATGAGATGCGCACTTGCCCAAGAAATGCGAG 300	
QY	301 GAGAGCAATATATGATGAAATTAATTAATTTCCCTTTGTTTAAATTTAGAAATTA 360	
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QY	361 ATGAGACCAAAATCAATGAATAGAAACAGCTCAGAAACAAAGATGTTTCCAATGG 420	
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DB	421 TAAATTAAGTATTTGTTCTTGGGAGAGAGCTCCATGTGATGCTTAATGAGAAATGGGAA 480	
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DB	481 AAAGCTCAAAAGCATGATGATGATGATCCCAAGTGAATTAATTTTAAATTAACCAT 540	
QY	541 GGCATCACTCTGGGAGAGCAAGTTCAGAAAGTTCATGTTAGCAAGAGATTAACATTAAC 600	
DB	541 GGCATCACTCTGGGAGAGCAAGTTCAGAAAGTTCATGTTAGCAAGAGATTAACATTAAC 600	
QY	601 AGCAAAATCAAAATTTCCGCAAAATGCAAGAGAAATGCGGACTGGGAAAGCTTTATTAAC 660	
DB	601 AGCAAAATCAAAATTTCCGCAAAATGCAAGAGAAATGCGGACTGGGAAAGCTTTATTAAC 660	
QY	661 AGTATTAAGGCAAGTTCATGTTGCAACACTCCCGCTTAATACAGAGAGCAACAAA 720	
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QY	901 TTGAAGATCATGAATTTTAAACATTTTAAGTAAACAAATATGCGATGATATGAG 960	
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QY	961 TTGAAGATCATGAATTTTAAAGTCAAGGATATACAGATATGCTGCTCCAGCTCC 1020	
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QY	1081 TGTATAGGCTTCACACACAGAGCCGATGTGTGACCTAACCAACATCTAACCCAA 1140	
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Db 2401 CCGAAGAAAGAAATGAGAGAGGAAATAGTCTAACGGAATCTGAGAGGAGCAAGTCTTC 2460
QY 2461 CTGAGAGGAGAAAGGAGCTCAAGTCCAGAGAAATTCAGAGAGTGGGAGCTGAGAGGAG 2520
Db 2461 CTGAGAGGAGAAAGGAGCTCAAGTCCAGAGAAATTCAGAGAGTGGGAGCTGAGAGGAG 2520
QY 2521 TGGGAGCGCTGGGAGCTGAGCGGAGTGTGAAAGCGAGAGGTGAAAGGCAAGCTGAA 2580
Db 2521 TGGGAGCGCTGGGAGCTGAGCGGAGTGTGAAAGCGAGAGGTGAAAGGCAAGCTGAA 2580
QY 2581 GCTGCCAGATGTTCAAGTGTGTGTGACGAGGAGTGGAGATTTCCGTTGCTTCGTGAGC 2640
Db 2581 GCTGCCAGATGTTCAAGTGTGTGTGACGAGGAGTGGAGATTTCCGTTGCTTCGTGAGC 2640
QY 2641 CTTTTATCTTTCTCTGCTTGGAGAGAGAGTCTAATTCATGAAGGAGTGAAGTTC 2700
Db 2641 CTTTTATCTTTCTCTGCTTGGAGAGAGAGTCTAATTCATGAAGGAGTGAAGTTC 2700
QY 2701 ATTAAGTACGCTGTAAATTCAGAGGAGTGGAGTGGTTCCTTCAAGAGCCTTTAT 2760
Db 2701 ATTAAGTACGCTGTAAATTCAGAGGAGTGGAGTGGTTCCTTCAAGAGCCTTTAT 2760
QY 2761 TTAATGGAAATATAGAGAGCAGCTCATTTCTAGGCGTAAATTCAGAGAAAGTGAAC 2820
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Db 2821 TGGAGTCTTTCTTCAATGCTCTTGGGCAACTACTAGCCGTGTGAGACTTGGCTTA 2880
QY 2881 TGCAGAGCGTGAAGAACTTGAATCAGAGACTCGGTTTTCTTCTGTTCTGCAATT 2940
Db 2881 TGCAGAGCGTGAAGAACTTGAATCAGAGACTCGGTTTTCTTCTGTTCTGCAATT 2940
QY 2941 GGTGGCTGTGAGACCGTGGCAAGTGTCTCTCTTCCCTGAGCAATGCTTCTGTCT 3000
Db 2941 GGTGGCTGTGAGACCGTGGCAAGTGTCTCTCTTCCCTGAGCAATGCTTCTGTCT 3000
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Db 3001 ATTAAGACCTTTGAGCTCTGTCTTCTGTAACACTTCCCTGTAATCTCTGTGAGGG 3060
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Db 3121 GGAAGAGAGGAGAGAGAGAGAGAGTGGTGTCTCATGATCTCATGATCATGATCATC 3180

QY 3181 CAGAGCCGAGAGCCAAATGCTTTCAGAGAAAGTCAATGAAACCCAAAGCCATTTTCT 3240
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QY 3241 TCCCTTACGATGAGCAATGGCATTTTCCCATTAACCAAAAGATGAGAGCTTAAGTGT 3300
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QY 3421 AGTACCTGAGAGGAG 3480
Db 3421 AGTACCTGAGAGGAG 3480
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QY 3541 GTTCTAG 3600
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QY 3721 GAGATTAGCAGCAAGAGGCAATCCGTTCTTTAAAGAGAAAGAAATCTCCTAAGAG 3780
Db 3721 GAGATTAGCAGCAAGAGGCAATCCGTTCTTTAAAGAGAAAGAAATCTCCTAAGAG 3780
QY 3781 TAAAGCCAAACAGATTGAAGCTTGAAGTCTTGAAGTCTTGAAGTCTTGAAGT 3840
Db 3781 TAAAGCCAAACAGATTGAAGCTTGAAGTCTTGAAGTCTTGAAGTCTTGAAGT 3840
QY 3841 CATTCAGAGATTTTCTAATGATTCAGAAATGAGCTGATCCCTTGGTGAAGT 3900
Db 3841 CATTCAGAGATTTTCTAATGATTCAGAAATGAGCTGATCCCTTGGTGAAGT 3900
QY 3901 TAAACAAACCCAGTTGAATGTCTCAAGTTCAAGCTTAACTGAGAACCAATCAAA 3960
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QY 3961 AGAATGAATCTTGAAGCAAACTGTGTTTCCCAATCTGAGAGTGAAGTCCAGAGG 4020
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QY 4021 AGTTGGAATATTTTCACTTCAAGATTTGACAGTGTGTGTGAATTAACAATTAAGT 4080
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Db 4081 TGCCTAAAGCAATCATTAATTTCAAGTGGCTTAAAGTTACTTCAAGCTTGTGTATAT 4140
QY 4141 TTAATGGCTATTTGCAATTTGCTTTTGTGTTTCTTGGTGTGATTAATTAAGTAAAGAG 4200
Db 4141 TTAATGGCTATTTGCAATTTGCTTTTGTGTTTCTTGGTGTGATTAATTAAGTAAAGAG 4200
QY 4201 GGAATTTAACTCAAGTCCAGAAAGCCGTGTAATTTGAAGAGAGAAATTTCAATTT 4260
Db 4201 GGAATTTAACTCAAGTCCAGAAAGCCGTGTAATTTGAAGAGAGAAATTTCAATTT 4260
QY 4261 TGTTTTACCACTTCTAACTTAATTAATTAATTTTCAATTTGAGATTAAGCATTA 4320

Db	4261	TGTTTTCACACCTTCTAATCTAAATTTACATTTTATCTCATTTGGCAATAGACCAATTA	4320
QY	4321	CTCAAAAGTGTAATTAACAGTACTGTGATTTGTCAATTTACCAATAGAAATCACAGACAT	4380
Db	4321	CTCAAAAGTGTAATTAACAGTACTGTGATTTGTCAATTTACCAATAGAAATCACAGACAT	4380
QY	4381	TTTATCTATATTAACAGTCTTGCGAGAACCTGTGAAGTGAATATTTATCTCAAAAGTA	4440
Db	4381	TTTATCTATATTAACAGTCTTGCGAGAACCTGTGAAGTGAATATTTATCTCAAAAGTA	4440
QY	4441	CTTTGAATTAAGACCTCTGCTGATCTTGTTTTAAACATATTAATTAACCATGTTTAA	4500
Db	4441	CTTTGAATTAAGACCTCTGCTGATCTTGTTTTAAACATATTAATTAACCATGTTTAA	4500
QY	4501	ATTTTGATTTTGTATATATCATATTTATATACATTTTGTCTTGTGTAATCTATATTTT	4560
Db	4501	ATTTTGATTTTGTATATATCATATTTATATACATTTTGTCTTGTGTAATCTATATTTT	4560
QY	4561	ATATATTTGAAAACATCTTTCTGAGAAGTCTCCAGATTTCCACAAATAGGTTCTTGG	4620
Db	4561	ATATATTTGAAAACATCTTTCTGAGAAGTCTCCAGATTTCCACAAATAGGTTCTTGG	4620
QY	4621	CATGCACACACACAGAGTAGAAGCTGATTTAGAGGCTTAACATTTGACATTTGTGCTCGAGA	4680
Db	4621	CATGCACACACACAGAGTAGAAGCTGATTTAGAGGCTTAACATTTGACATTTGTGCTCGAGA	4680
QY	4681	TGCAAGACTGAAATTAGAAAGTTCTCCCAAGATACACAGTGTTTTAAAGCTAGAGGCTG	4740
Db	4681	TGCAAGACTGAAATTAGAAAGTTCTCCCAAGATACACAGTGTTTTAAAGCTAGAGGCTG	4740
QY	4741	AGGGGGGAAATCTGCCGCTTCTATAGAAATGCTCTCCCTGAGCTGAGTGGTGTCTGC	4800
Db	4741	AGGGGGGAAATCTGCCGCTTCTATAGAAATGCTCTCCCTGAGAGCTGAGTGGTGTCTGC	4800
QY	4801	CTTGTGTCTGAGCTGGCTGTATTTTCTCTGTCGCGCTACAGCTTAATTAAGGACTGTGTT	4860
Db	4801	CTTGTGTCTGAGCTGGCTGTATTTTCTCTGTCGCGCTACAGCTTAATTAAGGACTGTGTT	4860
QY	4861	GGATCTCCAGTCTCCTAGCATAGTGTGCTGCGACAGTGCAGAGTTCATAGACTTTGCAG	4920
Db	4861	GGATCTCCAGTCTCCTAGCATAGTGTGCTGCGACAGTGCAGAGTTCATAGACTTTGCAG	4920
QY	4921	TGAATGGAATATTAACACTAGAAATATATCTTTGTGAATATGACACACCAATAGCTCGG	4980
Db	4921	TGAATGGAATATTAACACTAGAAATATATCTTTGTGAATATGACACACCAATAGCTCGG	4980
QY	4981	TGTAGTGTGTGTATGCTGT	5040
Db	4981	TGTAGTGTGTGTATGCTGT	5040
QY	5041	TAGGAATAATTAATGGGGTAGTGAGTGCATAAATTTGGATGTTCTTTTAAAAAGAACTC	5100
Db	5041	TAGGAATAATTAATGGGGTAGTGAGTGCATAAATTTGGATGTTCTTTTAAAAAGAACTC	5100
QY	5101	CAAAACAGACTTGTGAAGGTTATTTTCTTAAGAACTTCTGTGCGACGCGTGAAGGCAACCC	5160
Db	5101	CAAAACAGACTTGTGAAGGTTATTTTCTTAAGAACTTCTGTGCGACGCGTGAAGGCAACCC	5160
QY	5161	CTGTGTGACAGCCCAACCCAGCTCAAGTGTGACCTGTCTTCTTCCCAATGAAGGCTG	5220
Db	5161	CTGTGTGACAGCCCAACCCAGCTCAAGTGTGACCTGTCTTCTTCCCAATGAAGGCTG	5220
QY	5221	GCTCCCACTATATATTAACCTCTCTGAGAGCTCGGAGCATAGACGACGACGAGG	5281
Db	5221	GCTCCCACTATATATTAACCTCTCTGAGAGCTCGGAGCATAGACGACGACGAGG	5281

Key	Location/Qualifiers
mutation	replace(4256, G)
mutation	/*tag= d
mutation	/note= "TIGRmt4 mutant"
mutation	replace(4337, G)
mutation	/*tag= a
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mutation	replace(4950, T)
mutation	/*tag= b
mutation	/note= "TIGRmt2 mutant"
mutation	4998
mutation	/*tag= c
mutation	/note= "TIGR added to produce TIGRmt3 mutant"
mutation	replace(5113, C)
mutation	/*tag= e
mutation	/note= "TIGRmt1 mutant"
20-OCT-2000 (first entry)	
A TIGR (trabecular meshwork inducible glucocorticoid receptor) promoter.	
TIGR: trabecular meshwork inducible glucocorticoid receptor; promoter;	
glaucoma; steroid sensitivity; progressive ocular hypertension;	
vision loss; ss.	
Homo sapiens.	
11-JAN-2000; 2000MO-US000559.	
11-JAN-1999; 99US-00227881.	
07-MAY-1999; 99US-00306828.	
(REGC) UNIV CALIFORNIA.	
Nguyen TD, Polansky JR, Chen P, Chen H;	
WPI; 2000-491060/43.	
Diagnosis, prognosis and treatment of glaucoma, based on detecting	
inducible glucocorticoid receptor gene.	
Claim 79; Page 117-119; 122PP; English.	
The present sequence represents a TIGR (trabecular meshwork inducible	
glucocorticoid receptor) promoter, isolated from an individual without	
glaucoma. The specification describes a method for the diagnosis,	
prognosis and treatment of glaucoma, based on detecting specific	
polymorphisms in the promoter of the TIGR gene. The method is used for	
diagnosis and prognosis of glaucoma (of all types), steroid sensitivity	
and progressive ocular hypertension that leads to loss of vision	
Glaucoma can be treated by administering an agent that binds to cis-	
acting elements within the TIGR promoter. The TIGR promoter (or other	
regulatory regions) can be used to express homologous or heterologous	
genes, particularly for tissue-specific expression of therapeutic	
transgenes for treating glaucoma, also to generate transgenic animals and	
in screening for compounds (specific modulators) with diagnostic or	
therapeutic potential. Fragments of the TIGR sequence can be used as	
amplification primers or probes, e.g. for isolating related sequences in	
non-human animals	
Sequence 5271 BP; 1476 A; 1138 C; 1231 G; 1426 T; 0 U; 0 Other;	

Db	1	ATCTTTGTTCACTTACCTCAGGGCTTTATGAAATGAATAGATTAACCAATGTGAAG	60
QY	61	TCCTATTAACCTGATAGCCTCCATTCGATGATATGCTTTGGCAGATGATMAAGATCA	120
Db	61	TCCTATTAACCTGATAGCCTCCATTCGATGATATGCTTTGGCAGATGATMAAGATCA	120
QY	121	GGAAAGAGATATCCACGTTAGCCAAAGTGTCCAGGCTGTGTCTTATTTTACTGA	180
Db	121	GGAAAGAGATATCCACGTTAGCCAAAGTGTCCAGGCTGTGTCTTATTTTACTGA	180
QY	181	CAGATGTGTCTCTGACAGAGCTATTTCTTCAGAAACATCATCCAAATGCTAATC	240
Db	181	CAGATGTGTCTCTGACAGAGCTATTTCTTCAGAAACATCATCCAAATGCTAATC	240
QY	241	CATCAACAGAGACTAAGAAACAGAAATGAGATGGGCCTTGCCAGAAAAATGCGAC	300
Db	241	CATCAACAGAGACTAAGAAACAGAAATGAGATGGGCCTTGCCAGAAAAATGCGAC	300
QY	301	GAGAGCAAAATATGATGAATAAATCTTTCCCTTGTTGTTTATTTACGAAAAAATG	360
Db	301	GAGAGCAAAATATGATGAATAAATCTTTCCCTTGTTTATTTACGAAAAAATG	360
QY	361	ATGAGACCAAAATCAATGATATAGGAAACAGCTCAGAAAAAAGATGTTCCAAATTGG	420
Db	361	ATGAGACCAAAATCAATGATATAGGAAACAGCTCAGAAAAAAGATGTTCCAAATTGG	420
QY	421	TAATTAATGATTTTGTCCTTGCGGAAAGACCTCCATGTGACTGATGGGAAATGGGA	480
Db	421	TAATTAATGATTTTGTCCTTGCGGAAAGACCTCCATGTGACTGATGGGAAATGGGA	480
QY	481	AAACGTCAAAAGCATGATCTGATCAGATCCCAAGTGTGATTTATTTAAAAACGAT	540
Db	481	AAACGTCAAAAGCATGATCTGATCAGATCCCAAGTGTGATTTATTTAAAAACGAT	540
QY	541	GGCATCTCTGGGGAGGGAAGTTGAGAAAGTCTATGTAGCAAAAGCATTAACAATAAC	600
Db	541	GGCATCTCTGGGGAGGGAAGTTGAGAAAGTCTATGTAGCAAAAGCATTAACAATAAC	600
QY	601	AGCAAAATCAAAATTTCCGCAAAATGCAAGAGGAAATGGGACTGGGAAACCTTTCTAAC	660
Db	601	AGCAAAATCAAAATTTCCGCAAAATGCAAGAGGAAATGGGACTGGGAAACCTTTCTAAC	660
QY	661	AGTATTAAGCAAGTTACCATGTTGGCAACCTCCCGTCTATACAGGGAACACAAA	720
Db	661	AGTATTAAGCAAGTTACCATGTTGGCAACCTCCCGTCTATACAGGGAACACAAA	720
QY	721	ATTGACTGGGCTAAGCCTGACCTTCAAGGGGAAATATGAAAACTGAGAGCAAAACAAA	780
Db	721	ATTGACTGGGCTAAGCCTGACCTTCAAGGGGAAATATGAAAACTGAGAGCAAAACAAA	780
QY	781	GACATGTTAAAAGGCACAGAACATTTGTAGGCTTCAAGAGCAGTGCCTCCAGCA	840
Db	781	GACATGTTAAAAGGCACAGAACATTTGTAGGCTTCAAGAGCAGTGCCTCCAGCA	840
QY	841	GGGACCTGAGGATTTGCTTTAGAGGGCACTTTCTTAAGGAATCTTAAGAAATC	900
Db	841	GGGACCTGAGGATTTGCTTTAGAGGGCACTTTCTTAAGGAATCTTAAGAAATC	900
QY	901	TTGAAAGATCATGATTTTAACTTTAATTAATAAACAATATCGATGCAATATCAG	960
Db	901	TTGAAAGATCATGATTTTAACTTTAATTAATAAACAATATCGATGCAATATCAG	960
QY	961	TTTAGACATGGGTCCCAATTTTATAAGTCAAGGATCAAGGATTAACGTGCCAGCTCC	1020
Db	961	TTTAGACATGGGTCCCAATTTTATAAGTCAAGGATCAAGGATTAACGTGCCAGCTCC	1020
QY	1021	GGATAGGTCAAGAAATCATTAAGAAACACTGTGTCCCATCTTAACCTTTTCAGAAATGATC	1080
Db	1021	GGATAGGTCAAGAAATCATTAAGAAACACTGTGTCCCATCTTAACCTTTTCAGAAATGATC	1080
QY	1081	TGTCAATAGCCTTCAACACAGGCCGATGTGTGACTTCAACCAACATCTCAACCCCA	1140

Ds	1081	IGTCATAGCCCTCACACACAGGCCCGGATGTCTCTGACCTCAACCACTCATTCAGAACCCAA	1140
Qy	1141	GTGCTTCACACATTGTTAAGCGTGCATCTCAGTAGGTGCCATTAACAAATGSCACTCCGCC	1200
Ds	1141	GTGCTTCACACATTGTTAAGCGTGCATCTCAGTAGGTGCCATTAACAAATGSCACTCCGCC	1200
Qy	1201	TGTGACGCCATCCCGCTCCACAGGAATCTCCCACTTAGACTTGTGCATCAGATGT	1260
Ds	1201	TGTGACGCCATCCCGCTCCACAGGAATCTCCCACTTAGACTTGTGCATCAGATGT	1260
Qy	1261	TACAGCCAGGAAGTCCGTGAGAGGTGAGGGTGTGTCTTACACTACCTGATGATCTTAC	1320
Ds	1261	TACAGCCAGGAAGTCCGTGAGAGGTGAGGGTGTGTCTTACACTACCTGATGATCTTAC	1320
Qy	1321	ACCTGAGCTCATCTGCACACCTCTGCTCCAGAGTTCAAGCAATTCCTGTCTACGCCCTCC	1380
Ds	1321	ACCTGAGCTCATCTGCACACCTCTGCTCCAGAGTTCAAGCAATTCCTGTCTACGCCCTCC	1380
Qy	1381	CGCGTAGTGGAGCTACAGCGCGACGCCCGGCTAATTTGTATGTTAGTAGAGATGG	1440
Ds	1381	CGCGTAGTGGAGCTACAGCGCGACGCCCGGCTAATTTGTATGTTAGTAGAGATGG	1440
Qy	1441	GTTCACCAATTAAGCCCGGCTGTCTTGAACCTGCACTCAGTCAGTATCACCACTCC	1500
Ds	1441	GTTCACCAATTAAGCCCGGCTGTCTTGAACCTGCACTCAGTATCACCACTCC	1500
Qy	1501	AGCCTCCCTAAAGTCTGGGATTAAGGCAATGATCACCCGCGCCGCAAGGTCAGTGT	1560
Ds	1501	AGCCTCCCTAAAGTCTGGGATTAAGGCAATGATCACCCGCGCCGCAAGGTCAGTGT	1560
Qy	1561	TTAATTAAGGAATACTGAATGTGTTTCTAAACCAACAGGAGAAACAGACAAAGCTGTGA	1620
Ds	1561	TTAATTAAGGAATACTGAATGTGTTTCTAAACCAACAGGAGAAACAGACAAAGCTGTGA	1620
Qy	1621	TAATTTCAAGGATTTCTGGGATGGGGAATGTGCATGAGCTGCTGCCTAGTCCAGAC	1680
Ds	1621	TAATTTCAAGGATTTCTGGGATGGGGAATGTGCATGAGCTGCTGCCTAGTCCAGAC	1680
Qy	1681	CACGTGTCCTCATCATTTCTCCCTCATCTCATATTTCAGGCTAAGTTACATTTATTT	1740
Ds	1681	CACGTGTCCTCATCATTTCTCCCTCATCTCATATTTCAGGCTAAGTTACATTTATTT	1740
Qy	1741	CACCATCTTTTGTGTGAAGCTTCCACATGTTACTGAATAAAGATATACATMAACTAG	1800
Ds	1741	CACCATCTTTTGTGTGAAGCTTCCACATGTTACTGAATAAAGATATACATMAACTAG	1800
Qy	1801	TTCCATTGGGGGCACTGTGTGTGTATTAAGGGAGAGGGCATTAACCCAGACTCCT	1860
Ds	1801	TTCCATTGGGGGCACTGTGTGTGTATTAAGGGAGAGGGCATTAACCCAGACTCCT	1860
Qy	1861	TGAAGCCCCCGGACAGAGGTTCCCTCTCCACGTGGGGAGCCCTGCAGACACCCGGGGTCC	1920
Ds	1861	TGAAGCCCCCGGACAGAGGTTCCCTCTCCACGTGGGGAGCCCTGCAGACACCCGGGGTCC	1920
Qy	1921	TGGGTGTCTCTGAGCAACTGTCCACGCCCGGTGCACATGTGTTTGTATATCATCTCTAGG	1980
Ds	1921	TGGGTGTCTCTGAGCAACTGTCCACGCCCGGTGCACATGTGTTTGTATATCATCTCTAGG	1980
Qy	1981	GACCTGTGTCTTCTAATTTCTGTGACTGTGTCAATTCACAGGAGATCATTGACAATT	2040
Ds	1981	GACCTGTGTCTTCTAATTTCTGTGACTGTGTCAATTCACAGGAGATCATTGACAATT	2040
Qy	2041	TATTGAGTACTTATATCTGCAGACACCAAGACAAATGTTGAGCAAGCATCACTGC	2100
Ds	2041	TATTGAGTACTTATATCTGCAGACACCAAGACAAATGTTGAGCAAGCATCACTGC	2100
Qy	2101	CTTACCTTGTTGAGAGGTGAAGTTTCTCATGGAAGCGTGCAGAAAGAAATTAATAGCCA	2160
Ds	2101	CTTACCTTGTTGAGAGGTGAAGTTTCTCATGGAAGCGTGCAGAAAGAAATTAATAGCCA	2160
Qy	2161	GCCCACTTAAACCCAGTGTGTAAGAAAGAAATTAACACATCTTGAAGAAATTGTGGCC	2220
Ds	2161	GCCCACTTAAACCCAGTGTGTAAGAAAGAAATTAACACATCTTGAAGAAATTGTGGCC	2220

QY 2221 AGCATCCCTTAACAAAGGACACCTCCCTAGACGCCCCCTGCTGCCTCATCTGTCCCGAGG 2280
 Db 2221 AGATCCCTTAACAAAGGCCACCTCCCTAGACGCCCCCTGCTGCCTCATCTGTCCCGAGG 2280
 QY 2281 CCCCAGGCCCCAGTCTTCAAGCCTCTCTCCATCAAGTCAAGCCTGAGCTGAGCTCT 2340
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 QY 2341 GCGTGGCTCCCGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400
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 QY 3181 CAGACGAGAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 3240
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 QY 3901 TAAACCAACAG 3960
 Db 3901 TAAACCAACAG 3960
 QY 3961 AGATTTGAATTTTAAAG 4020
 Db 3961 AGATTTGAATTTTAAAG 4020
 QY 4021 AGTTTGAATTTTAAAG 4080
 Db 4021 AGTTTGAATTTTAAAG 4080
 QY 4081 TGGTCAAG 4140
 Db 4081 TGGTCAAG 4140
 QY 4141 TTATTTGCTAATTTTAAAG 4200
 Db 4141 TTATTTGCTAATTTTAAAG 4200
 QY 4201 GATTTTAAATTTTAAAG 4260
 Db 4201 GATTTTAAATTTTAAAG 4260
 QY 4261 TGTTTTAAACCTTTTAAAG 4320
 Db 4261 TGTTTTAAACCTTTTAAAG 4320
 QY 4321 CTCAAGTGTATTAACAG 4380
 Db 4321 CTCAAGTGTATTAACAG 4380
 QY 4381 TTATTTAATTTTAAAG 4440
 Db 4381 TTATTTAATTTTAAAG 4440

[illegible]

OS	Homo sapiens.
XX	
PN	W09832850-A1.
PD	30-JUL-1998.
PF	09-JAN-1998; 98WC-US6000468.
XX	
PR	28-JAN-1997; 57US-00791154.
PA	26-SEP-1997; 97US-00938669.
XX	
PI	(REGC) UNIV CALIFORNIA.
DR	Nguyen TD, Polansky JR, Chen P, Chen H;
XX	WPI; 1998-427846/35.
PT	Use of TIGR nucleic acid sequences - used for, e.g. developing products
PS	for diagnosis, prognosis and treatment of glaucoma.
XX	
CC	Claim 34; Fig 1; 105pp; English.
CC	This sequence is a trabecular meshwork induced glucocorticoid response
CC	protein (TIGR) promoter region which is used in a method for diagnosing
CC	glaucoma in a patient. The method involves the detection of polymorphisms
CC	whose presence is predictive of a mutation affecting TIGR response in the
CC	patient and can be diagnostic of glaucoma or steroid sensitivity. Base
CC	substitutions and base additions upstream of and within TIGR exons can
CC	also be used to diagnose glaucoma
XX	
SQ	Sequence 5299 BP; 1482 A; 1151 C; 1235 G; 1431 T; 0 U; 0 Other;
Query Match	99.5%; Score 5246.4; DB 2; Length 5299;
Best Local Similarity	99.9%; Pred. No. 0;
Matches 5269; Conservative	0; Mismatches 1; Indels 2; Gaps 2
OY	1 ATCTTTGTCAGTTTACCTCGAGGGCTATTATGAATAAGAAATGCAATGTGAAG 60
DB	1 ATCTTTGTCAGTTTACCTCGAGGGCTATTATGAATAAGAAATGCAATGTGAAG 60
OY	61 TCCATTAATGTAATGCCTCCATTCGGATGTATGCTTGAGAGATGATTAAGAATCA 120
DB	61 TCCATTAATGTAATGCCTCCATTCGGATGTATGCTTGAGAGATGATTAAGAATCA 120
OY	121 GGAAGAGAGATGCCAGCTTAGCCAAAGTGTCCAGGCTGTCTCTTAATTTACTGA 180
DB	121 GGAAGAGAGATGCCAGCTTAGCCAAAGTGTCCAGGCTGTCTCTTAATTTACTGA 180
OY	181 CAATGTGTGCTCTGACAGAACCTTCTTCAGAAACATACATCCAAATGCTAATC 240
DB	181 CAATGTGTGCTCTGACAGAACCTTCTTCAGAAACATACATCCAAATGCTAATC 240
OY	241 CATCAAAACAGAGCTAAGAAAACAGAAATGAGATGGGCACTTGCCCAAGAAAAATG 300
DB	241 CATCAAAACAGAGCTAAGAAAACAGAAATGAGATGGGCACTTGCCCAAGAAAAATG 300
OY	301 GAAGCAAAATATGATGAAAAATAAACCCTTTCCTGTTTAAATTCAGAAAAATG 360
DB	301 GAAGCAAAATATGATGAAAAATAAACCCTTTCCTGTTTAAATTCAGAAAAATG 360
OY	361 ATGAGAGCAAATATCAATCATATGAAATAGAAAAAGCTCAGAAAAAGATGTTCCAAATTGG 420
DB	361 ATGAGAGCAAATATCAATCATATGAAATAGAAAAAGCTCAGAAAAAGATGTTCCAAATTGG 420
OY	421 TAATTAAGTATTTGTTCTTGGAAAGAGACCTCCATGTGAGCTTGATGGAAAAATGGGAA 480
DB	421 TAATTAAGTATTTGTTCTTGGAAAGAGACCTCCATGTGAGCTTGATGGAAAAATGGGAA 480
OY	481 AAACGTCAAAACATGATCTGATGATCCCAAGTGGATTAATATTTTAAACAACGAT 540
DB	481 AAACGTCAAAACATGATCTGATGATCCCAAGTGGATTAATATTTTAAACAACGAT 540
OY	541 GGATCTACTCTGGGAGGCAATTGAGGAAGTCAATGTTAGCAAAAGACATAACATTAAC 6000

Db	541	GGCATCTACTCTGGGAGAGCGAAGTTCAAGAGAGTATGTTAGCAAAAGACATTAACATTAAC	600
Qy	601	AGCAAAATCAAAATTTCCGCAAAATGACAGAGGAAAATGGGAATGGGAAGCTTCAATTAAC	660
Db	601	AGCAAAATCAAAATTTCCGCAAAATGACAGAGGAAAATGGGAATGGGAAGCTTCAATTAAC	660
Qy	661	AGTATTAAGGACGTTGACCAATGTTGCGAACACCTCCCGCTGTATACCAAGGAAACACAAA	720
Db	661	AGTATTAAGGACGTTGACCAATGTTGCGAACACCTCCCGCTGTATACCAAGGAAACACAAA	720
Qy	721	ATTGACTGGGCTAAGCTGACCTTCAAGGAAATATGAAAACTGAGACAAACAAA	780
Db	721	ATTGACTGGGCTAAGCTGACCTTCAAGGAAATATGAAAACTGAGACAAACAAA	780
Qy	781	GACATGGTTAAAAGGCAACCAAGAACTTTGTAAGCTTCAAAAGCAGCACTGCCCCCTACGA	840
Db	781	GACATGGTTAAAAGGCAACCAAGAACTTTGTAAGCTTCAAAAGCAGCACTGCCCCCTACGA	840
Qy	841	GGGACCCCTGAGGCACTTGGCCCTTGAAGGAGCGACGTTTCTTAAGAAATCTTAAGAACTC	900
Db	841	GGGACCCCTGAGGCACTTGGCCCTTGAAGGAGCGACGTTTCTTAAGAAATCTTAAGAACTC	900
Qy	901	TTGAAGATCATGAATTTTAAACAATTTTAACTATTAACAAATAATGGCATATATCAG	960
Db	901	TTGAAGATCATGAATTTTAAACAATTTTAACTATTAACAAATAATGGCATATATCAG	960
Qy	961	TTTGAACATGGGTCCTCCAAATTTTATTAAGTCAAGCATACAGAAATTAAGTGTCCAGCTCC	1020
Db	961	TTTGAACATGGGTCCTCCAAATTTTATTAAGTCAAGCATACAGAAATTAAGTGTCCAGCTCC	1020
Qy	1021	GGATAGGTCAGAAATCATTTAGAAATCACTGTGCCCATCTCTAATCTTTTCAGATATATC	1080
Db	1021	GGATAGGTCAGAAATCATTTAGAAATCACTGTGTGCCCATCTCTAATCTTTTCAGATATATC	1080
Qy	1081	TGTCAATGACCTCTCAACAACAGGCCCGATGTGTGTGACCTTACAAACAACATCTTAAACCCA	1140
Db	1081	TGTCAATGACCTCTCAACAACAGGCCCGATGTGTGTGACCTTACAAACAACATCTTAAACCCA	1140
Qy	1141	GTCGCTCAACATTTGTTAAGCTGTATCTCAATGAGTCCCACTTCAAAATGCGACCTCCCC	1200
Db	1141	GTCGCTCAACATTTGTTAAGCTGTATCTCAATGAGTCCCACTTCAAAATGCGACCTCCCC	1200
Qy	1201	TGTGACGCCCATCCCGCTCCACAGAGAGTCTCCCATCTCTAAGCTTCTGCATCAACAATGT	1260
Db	1201	TGTGACGCCCATCCCGCTCCACAGAGAGTCTCCCATCTCTAAGCTTCTGCATCAACAATGT	1260
Qy	1261	TACAGCCAGAAAGCTCCGTGAGAGGTCTGTGTCTTAACTCACTGTATATGCTCTAC	1320
Db	1261	TACAGCCAGAAAGCTCCGTGAGAGGTCTGTGTCTTAACTCACTGTATATGCTCTAC	1320
Qy	1321	ACCTGAGTCACTGCGAACCTCTGCTCCCAAGTCAAGCAATTTCTCTGTCTCAGCCTCC	1380
Db	1321	ACCTGAGTCACTGCGAACCTCTGCTCCCAAGTCAAGCAATTTCTCTGTCTCAGCCTCC	1380
Qy	1381	CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTGTATTTGTTAGTAGAGATGGG	1440
Db	1381	CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTGTATTTGTTAGTAGAGATGGG	1440
Qy	1441	GTTTCACCAATTTAGCCCGCGCTGTCTTGAACCTCTGACCTCAAGTATCCACCACCTTC	1500
Db	1441	GTTTCACCAATTTAGCCCGCGCTGTCTTGAACCTCTGACCTCAAGTATCCACCACCTTC	1500
Qy	1501	AGCCTCTCAAAAGTGTGTGAGTTTACAGCATGATCACCGCGCCCGGCAAGAGTCAAGTGT	1560
Db	1501	AGCCTCTCAAAAGTGTGTGAGTTTACAGCATGATCACCGCGCCCGGCAAGAGTCAAGTGT	1560
Qy	1561	TTAATTAAGGAATTACTTGAATGTCTTACTTAAACCAACAGGGAACAGCAAAAGCTGTGA	1620
Db	1561	TTAATTAAGGAATTACTTGAATGTCTTACTTAAACCAACAGGGAACAGCAAAAGCTGTGA	1620
Qy	1621	TAAATTCAGGAGTTCTTGGGATGGGGAATGAGCATAGAGTGCCTGCTATGCTCCAGAC	1680

Db	162	TAAATTCAAGGAAATTCCTGGATGAGGGAATGATGCTCCATGAGACCTGCGCTAGTCCCAAC	1680
Oy	1681	CAGTGGTCTCACTACTTCTTCTCCCTCATCTCTATTTTCAAGGCTAAGTTACATTTTAT	1740
Db	1681	CAGTGGTCTCACTACTTCTTCTCCCTCATCTCTATTTTCAAGGCTAAGTTACATTTTAT	1740
Oy	1741	CACATGCTTTGTGTGTAGCCTCCACATGTTACTGAATATAGATATACATAAATCTAG	1800
Db	1741	CACATGCTTTGTGTGTAGCCTCCACATGTTACTGAATATAGATATACATAAATCTAG	1800
Oy	1801	TTTCATTTGGGSCCATCTGTGTGTGTATAGGGAAGAGGCAATPCCCCAGACCTCT	1860
Db	1801	TTTCATTTGGGSCCATCTGTGTGTGTATAGGGAAGAGGCAATPCCCCAGACCTCT	1860
Oy	1861	TGAAGCCCCGGGCAAGAGTTCTCTCCACATGGGGAAGCCCTGCAGAGACCCGGGCTC	1920
Db	1861	TGAAGCCCCGGGCAAGAGTTCTCTCCACATGGGGAAGCCCTGCAGAGACCCGGGCTC	1920
Oy	1921	TGGGTGTCTTGAGCAACCTGCAGACCCGTCACATGTTGTTTGTATCACTCTAGG	1980
Db	1921	TGGGTGTCTTGAGCAACCTGCAGACCCGTCACATGTTGTTTGTATCACTCTAGG	1980
Oy	1981	GACCTGTGTCTTTCTATTTCTGTGTACTGCTTATTCATCCAGGATTCATTTGCAATT	2040
Db	1981	GACCTGTGTCTTTCTATTTCTGTGTACTGCTTATTCATCCAGGATTCATTTGCAATT	2040
Oy	2041	TATTGAGTACTATATCTGCAGAGACACAGACAAATGTGTAGCAAGACGTACTGC	2100
Db	2041	TATTGAGTACTATATCTGCAGAGACACAGACAAATGTGTAGCAAGACGTACTGC	2100
Oy	2101	CCTACCTTGTTGAGAGTGAACATTTCTCATGTAGAAAGCTGTACAGAGAAATTAATAGCA	2160
Db	2101	CCTACCTTGTTGAGAGTGAACATTTCTCATGTAGAAAGCTGTACAGAGAAATTAATAGCA	2160
Oy	2161	GCCAACTTAAACCCAGTCTCTGAAGAAGAAATTAACCCATCTTGAAGATTGTGGG	2220
Db	2161	GCCAACTTAAACCCAGTCTCTGAAGAAGAAATTAACCCATCTTGAAGATTGTGGG	2220
Oy	2221	AGCATCCCTTAAACAAGGCACTCCCTAGAGGCCCTGTGCTCCATCGTCCCGAGAG	2280
Db	2221	AGCATCCCTTAAACAAGGCACTCCCTAGAGGCCCTGTGCTCCATCGTCCCGAGAG	2280
Oy	2281	CCCCCAAGCCGAGTCTTCCAGGCTCTCTCTCATATGTCACAGGCTGTGAGCTGGCT	2340
Db	2281	CCCCCAAGCCGAGTCTTCCAGGCTCTCTCTCATATGTCACAGGCTGTGAGCTGGCT	2340
Oy	2341	GCTCGCTTCCGCTGAATGCTCCGTGTGATCTGTGTGATCTGTGTGAGTCTCTTGCTCCAGGCT	2400
Db	2341	GCTCGCTTCCGCTGAATGCTCCGTGTGATCTGTGTGATCTGTGTGAGTCTCTTGCTCCAGGCT	2400
Oy	2401	CCAGAAAGGAAATGAGAGAGGAAATCTAGTCTAAACGAGAACTGTGAGGGGACAGTGTTC	2460
Db	2401	CCAGAAAGGAAATGAGAGAGGAAATCTAGTCTAAACGAGAACTGTGAGGGGACAGTGTTC	2460
Oy	2461	CTTACAGAGGAAAGGGGCTCCACATCCACAGAGAAATTCACAGAGAGTGGGACATGACAGGAG	2520
Db	2461	CTTACAGAGGAAAGGGGCTCCACATCCACAGAGAAATTCACAGAGAGTGGGACATGACAGGAG	2520
Oy	2521	TGGGAGAGCTGTGGGGCTGAGCGGGTGTCTGAAGGAGAAAGTGAATAAAGGCAAGGCTGA	2580
Db	2521	TGGGAGAGCTGTGGGGCTGAGCGGGTGTCTGAAGGAGAAAGTGAATAAAGGCAAGGCTGA	2580
Oy	2581	GCTGCCAGATGTTCAAGTGTGTTTCAAGGGGCTGGGATTTCCGTTGCTTCCGTGTAGC	2640
Db	2581	GCTGCCAGATGTTCAAGTGTGTTTCAAGGGGCTGGGATTTCCGTTGCTTCCGTGTAGC	2640
Oy	2641	CTTTTATCTTTCTCTGTGTGAGAGAGAAAGATCTATTTCAATGAAGGATGTAGCTTC	2700
Db	2641	CTTTTATCTTTCTCTGTGTGAGAGAGAAAGATCTATTTCAATGAAGGATGTAGCTTC	2700
Oy	2701	ATAAAGTCAAGTGTTPAAATTCAGAGGTGTGATGAGTGTCTTCTTCAAGAGGCTTTAT	2760
Db	2701	ATAAAGTCAAGTGTTPAAATTCAGAGGTGTGATGAGTGTCTTCTTCAAGAGGCTTTAT	2760

2761 TTAATGGGAATATAGAGACGAGCTCATTTCTAGGCCGTTAATTACAGGAAGAAGTAC 2820
Db TTAATGGGAATATAGGAACGAGCTCATTTCTAGGCCGTTAATTACAGGAAGAAGTAC 2820
Qy 2821 TGAAGCTTTTCTTTTATGTCTTTCTGGGCACTACTCAGCCTGTGTGAATCTGGCTTA 2880
Db 2821 TGAAGCTTTTCTTTTATGTCTTTCTGGGCACTACTCAGCCTGTGTGAATCTGGCTTA 2880
Qy 2881 TGAAGACGCTGCAAAACCTTGGAAATCAGAGACTCGGTTTCTTCTGTGTGTCATTT 2940
Db 2881 TGAAGACGCTGCAAAACCTTGGAAATCAGAGACTCGGTTTCTTCTGTGTGTCATTT 2940
Qy 2941 GGTGGCTGTGCGACCGTGGGCAAGTGTCTCTCTTCCCTGGGCCAATAGTCTTCTGCT 3000
Db 2941 GGTGGCTGTGCGACCGTGGGCAAGTGTCTCTCTTCCCTGGGCCAATAGTCTTCTGCT 3000
Qy 3001 ATAAAGACCTTGACAGCTGTGGTCTGTGTAACCTCCCTGATCTCTGTGAGGG 3060
Db 3001 ATAAAGACCTTGACAGCTGTGGTCTGTGTAACCTCCCTGATCTCTGTGAGGG 3060
Qy 3061 GGAATGTTAGAGAGGAGAGGACAGAGCTGAGACAGTGAACACAGGGGAGGTGAAGG 3120
Db 3061 GGAATGTTAGAGAGGAGAGGACAGAGCTGAGACAGTGAACACAGGGGAGGTGAAGG 3120
Qy 3121 GGAAGAGAGGAGAGGAGAGGAGTGGTGTCTCATAGTCTCATGATCAGTCAAGTCTC 3180
Db 3121 GGAAGAGAGGAGAGGAGAGGAGTGGTGTCTCATAGTCTCATGATCAGTCAAGTCTC 3180
Qy 3181 CAGGACCGAGAGGACCAATGCTTTCAGGAAAGCTCATGAAACCAACAGCCATTTTCT 3240
Db 3181 CAGGACCGAGAGGACCAATGCTTTCAGGAAAGCTCATGAAACCAACAGCCATTTTCT 3240
Qy 3241 TCCCTAGACATGACATGAGCTTTTCCCATTAACCAAAAGATGACAGACTAATCTGT 3300
Db 3241 TCCCTAGACATGACATGAGCTTTTCCCATTAACCAAAAGATGACAGACTAATCTGT 3300
Qy 3301 GGTAGCTTTTGGCTGGCATTTCAAAAAGTGGGCAAGCAAGTGAAGAAATGCAAGATTG 3360
Db 3301 GGTAGCTTTTGGCTGGCATTTCAAAAAGTGGGCAAGCAAGTGAAGAAATGCAAGATTG 3360
Qy 3361 TTAACCTTTTCAACCTGACAGACCCCAACGAGTCAAGTGAATGCTGACAGCAGG 3420
Db 3361 TTAACCTTTTCAACCTGACAGACCCCAACGAGTCAAGTGAATGCTGACAGCAGG 3420
Qy 3421 AGTGAACCTGACAGGAGGAGGAGAGAAAGAGAGGATAGTGAATGAGCAAGAAAG 3480
Db 3421 AGTGAACCTGACAGGAGGAGGAGAGAAAGAGAGGATAGTGAATGAGCAAGAAAG 3480
Qy 3481 ACAGATTCAATCAAGGAGAGTGGAAATGACCAAGGATTAATGTCACAGTGAATCTTG 3540
Db 3481 ACAGATTCAATCAAGGAGAGTGGAAATGACCAAGGATTAATGTCACAGTGAATCTTG 3540
Qy 3541 GTTCTAGAGGAGAGGCTTATTTGGGGGAGAAAAATCAAGTCAAGGAAAGTGGGAGA 3600
Db 3541 GTTCTAGAGGAGAGGCTTATTTGGGGGAGAAAAATCAAGTCAAGGAAAGTGGGAGA 3600
Qy 3601 CCGATTTCTAATATATATTTTCTTTTACAGGTGATTAATCTGAGCAAGTCAAG 3660
Db 3601 CCGATTTCTAATATATATTTTCTTTTACAGGTGATTAATCTGAGCAAGTCAAG 3660
Qy 3661 GTAGTACTGAGGCTGTAAATTAATTAATTTCTCTTATTAAGAACTCTTTTCTGT 3720
Db 3661 GTAGTACTGAGGCTGTAAATTAATTAATTTCTCTTATTAAGAACTCTTTTCTGT 3720
Qy 3721 GGAGTTAGAGACAAAGGCAATCCGTTCTTTTACAGGAAGAAACATTCCTAAG 3780
Db 3721 GGAGTTAGAGACAAAGGCAATCCGTTCTTTTACAGGAAGAAACATTCCTAAG 3780
Qy 3781 TAAAGCAAAAGATTCAGGCTAGCTTGTCTGATATATGATGTTTGTAAAAAT 3840
Db 3781 TAAAGCAAAAGATTCAGGCTAGCTTGTCTGATATATGATGTTTGTAAAAAT 3840

Qy 3841 CATTCAGAGATTTTACTATCTGATTCAGAAAAATGAGACTAGACCTTTGTGACGTC 3900
Db 3841 CATTCAGAGATTTTACTATCTGATTCAGAAAAATGAGACTAGACCTTTGTGACGTC 3900
Qy 3901 TTAACAAACCCAGTTTAAATGTCTCAAGTTAGGCTTAATCTGACAGAACCAATGAAA 3959
Db 3901 TTAACAAACCCAGTTTAAATGTCTCAAGTTAGGCTTAATCTGACAGAACCAATGAAA 3960
Qy 3960 AAGAATGAATCTTTAGAGCAACCTGTGTTCTCCATCTGAGAGGTGAGTGCAGAGG 4019
Db 3961 AAGAATGAATCTTTAGAGCAACCTGTGTTCTCCATCTGAGAGGTGAGTGCAGAGG 4019
Qy 4020 CAGTTGGAATATTTACTTACAGATTTGACACGCTGTGTGTATTAACAATTAAG 4079
Db 4020 CAGTTGGAATATTTACTTACAGATTTGACACGCTGTGTGTATTAACAATTAAG 4079
Qy 4080 TTGCTCAAGCAATCATTAATTTCAAGGCTTAAATGTTACTCTGACAGTTTGGTATA 4139
Db 4080 TTGCTCAAGCAATCATTAATTTCAAGGCTTAAATGTTACTCTGACAGTTTGGTATA 4139
Qy 4140 TTTATGGCTATGGCAATTTGTTTTTTTCTTTGGGTTTATATGTAAAGCA 4199
Db 4140 TTTATGGCTATGGCAATTTGTTTTTTTCTTTGGGTTTATATGTAAAGCA 4199
Qy 4200 GGGATTTAATACCTAGCTGAGAAAGCTGTGAATTTGAAATGAGAAAAATTAACATTT 4259
Db 4200 GGGATTTAATACCTAGCTGAGAAAGCTGTGTGATTTGAAATGAGAAAAATTAACATTT 4259
Qy 4260 TTGTTTATACACCTTCACTAAATTTAAATTTAATTCATTTGCGAATAGAGCCATA 4319
Db 4260 TTGTTTATACACCTTCACTAAATTTAATTTAATTCATTTGCGAATAGAGCCATA 4319
Qy 4320 ACTCAAAATGTTAATACAGTACTGTGATTTGTGCTTACCAATGAAATCAACACT 4379
Db 4320 ACTCAAAATGTTAATACAGTACTGTGATTTGTGCTTACCAATGAAATCAACACT 4379
Qy 4380 TTTATACTATATTTACAGTGTGAGATAGCTTGAATGAAATATTTATCTCAAAACT 4439
Db 4380 TTTATACTATATTTACAGTGTGAGATAGCTTGAATGAAATATTTATCTCAAAACT 4439
Qy 4440 ACTTGAATTTAGACCTCTGCTGAGATCTGTTTAAATTAATTAATTAATGTTTAA 4499
Db 4440 ACTTGAATTTAGACCTCTGCTGAGATCTGTTTAAATTAATTAATTAATGTTTAA 4499
Qy 4500 AATTTGATTTTGAATATCAATTTTCAATTTATTTCTTTGATTTGATTAATTT 4559
Db 4500 AATTTGATTTTGAATATCAATTTTCAATTTATTTCTTTGATTTGATTAATTT 4559
Qy 4560 TATATATTTGAAAAATCTTTCTGAGAAAGTTCACCAATTAAGAGTCTTG 4619
Db 4560 TATATATTTGAAAAATCTTTCTGAGAAAGTTCACCAATTAAGAGTCTTG 4619
Qy 4620 GCATGCAACACACAGGTAAAGATTAAGAGCTAATTAAGCAATTTGAGGCTGAG 4679
Db 4620 GCATGCAACACACAGGTAAAGATTAAGAGCTAATTAAGCAATTTGAGGCTGAG 4679
Qy 4680 ATGCAAGCTGAATTTGAAAGTTCACCAAGATTAAGAGTCTTTTAAAGTGAAGGCT 4739
Db 4680 ATGCAAGCTGAATTTGAAAGTTCACCAAGATTAAGAGTCTTTTAAAGTGAAGGCT 4739
Qy 4740 GAGGGGGGAAATCTGCGCTTCTATAGAAATGCTTCCCTGAGGCTGTAGGGTGTCT 4799
Db 4740 GAGGGGGGAAATCTGCGCTTCTATAGAAATGCTTCCCTGAGGCTGTAGGGTGTCT 4799
Qy 4800 CTTGTGTTCTGCTGCTGTATTTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4859
Db 4800 CTTGTGTTCTGCTGCTGTATTTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4859
Qy 4860 TGAATCTCAAGTCTTACATAGTCTGAGACAGTGAAGTCTTCAATAGATTTGACAA 4919
Db 4860 TGAATCTCAAGTCTTACATAGTCTGAGACAGTGAAGTCTTCAATAGATTTGACAA 4919
Qy 4920 GTGAATGGAATATTAACCTGAAATATATATCTGTTGAAATAGCACACAGATGCTG 4979

Db 601 AGCAAAATCAAATTTCCGAAATTCAGAGGAAAAATGGGACTGGGAAAGCTTTCATTAAC 660
Qy 661 AGTATTAGGCACTTACCATGTTGCGCAACACCTCCCGTCTATACGAGGAAACAAAA 720
Db 661 AGTATTAGGCACTTACCATGTTGCGCAACACCTCCCGTCTATACGAGGAAACAAAA 720
Qy 721 ATTGACTGGGCTAAGCTGGACTTTTCAGAGGAAATATGAAAAATCGAGAGGAAACAAAA 780
Db 721 ATTGACTGGGCTAAGCTGGACTTTTCAGAGGAAATATGAAAAATCGAGAGGAAACAAAA 780
Qy 781 GACATGTTTAAAGGCAACAGAAATTTGAGCCTTCMAAGCAGCAGTCCCTCAGCA 840
Db 781 GACATGTTTAAAGGCAACAGAAATTTGAGCCTTCMAAGCAGCAGTCCCTCAGCA 840
Qy 841 GGGACCTTAGGATTTGCTTTAGAGGCGAGTTTCTTAAGGAATCTTAAGAACTC 900
Db 841 GGGACCTTAGGATTTGCTTTAGAGGCGAGTTTCTTAAGGAATCTTAAGAACTC 900
Qy 901 TTGAAAGATCATGATTTTACCATTTTAAGTATTAACAAATATGCGATGCAATATCAG 960
Db 901 TTGAAAGATCATGATTTTACCATTTTAAGTATTAACAAATATGCGATGCAATATCAG 960
Qy 961 TTTAGACATGGGTCCCAATTTTATAAGTCAGGCAATACAGGATACGCTGCCAGCTCC 1020
Db 961 TTTAGACATGGGTCCCAATTTTATAAGTCAGGCAATACAGGATACGCTGCCAGCTCC 1020
Qy 1021 GGATAGGTGAGAAATCATTAAGAAATCACTGTCCTCCATCCCTAATTTTTCAGAAATATC 1080
Db 1021 GGATAGGTGAGAAATCATTAAGAAATCACTGTCCTCCATCCCTAATTTTTCAGAAATATC 1080
Qy 1081 TGTGATAGCTCTGACACACAGGCGGATGTGTCTGACTTACACACATCTCAACCCAA 1140
Db 1081 TGTGATAGCTCTGACACACAGGCGGATGTGTCTGACTTACACACATCTCAACCCAA 1140
Qy 1141 GTGGCTCAACCATTTGTTAAAGTCATGTCAGTGGTCCCATCTTCAATATGCACTCC 1200
Db 1141 GTGGCTCAACCATTTGTTAAAGTCATGTCAGTGGTCCCATCTTCAATATGCACTCC 1200
Qy 1201 TGTGACGCCCATCCGCTCCACAGGAAGTCTCCCATCTAGACTTGTGATCAGATGT 1260
Db 1201 TGTGACGCCCATCCGCTCCACAGGAAGTCTCCCATCTAGACTTGTGATCAGATGT 1260
Qy 1261 TACAGCAAAAGCTCCGAGGAGTGGGTCTGTCTTACACCTACCTGTATGCTCTTAC 1320
Db 1261 TACAGCAAAAGCTCCGAGGAGTGGGTCTGTCTTACACCTACCTGTATGCTCTTAC 1320
Qy 1321 ACCTGAGCTCATGCAACCTGCTCTCCAGGTTCAAGCAATTCCTGCTCAGCTCC 1380
Db 1321 ACCTGAGCTCATGCAACCTGCTCTCCAGGTTCAAGCAATTCCTGCTCAGCTCC 1380
Qy 1381 CCGGTAGCTGGGACTACAGGCGCAGCCCGGCTAATTTTGTATTTAGTATGATGGG 1440
Db 1381 CCGGTAGCTGGGACTACAGGCGCAGCCCGGCTAATTTTGTATTTAGTATGATGGG 1440
Qy 1441 GTTTCACATATTAGCCGCTGTGTCTGAACCTGTAACCTCAGGTATCAACCACTC 1500
Db 1441 GTTTCACATATTAGCCGCTGTGTCTGAACCTGTAACCTCAGGTATCAACCACTC 1500
Qy 1501 AACCTCTTAAAGTCTGGGATTAACAGCATGATCAACGCGCCGCGCAAGGCTCAGTG 1560
Db 1501 AACCTCTTAAAGTCTGGGATTAACAGCATGATCAACGCGCCGCGCAAGGCTCAGTG 1560
Qy 1561 TTAATTAAGGAATTAAGTAAATGTTTAAACCAACAGGGAACACAAAGCTGTGA 1620
Db 1561 TTAATTAAGGAATTAAGTAAATGTTTAAACCAACAGGGAACACAAAGCTGTGA 1620
Qy 1621 TAAATTTCAAGGATTTCTGGGATGGGGAATGATGATGCTGCTGCTGCTGCTGCTGCTG 1680
Db 1621 TAAATTTCAAGGATTTCTGGGATGGGGAATGATGATGCTGCTGCTGCTGCTGCTGCTG 1680
Qy 1681 CACTGCTCTATCACTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740
Db 1681 CACTGCTCTATCACTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740

Db 1681 CACTGCTCTATCACTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740
Qy 1741 CACCATGCTTTTGTGTAGGCTTCCACATGCTTACTGAAATTAAGATATCATTAACCTAG 1800
Db 1741 CACCATGCTTTTGTGTAGGCTTCCACATGCTTACTGAAATTAAGATATCATTAACCTAG 1800
Qy 1801 TTCATTTGGGGCCATCTGTGTGTGTATGAGGAGAGAGGAGATCCCAAGAGCTCT 1860
Db 1801 TTCATTTGGGGCCATCTGTGTGTGTATGAGGAGAGAGGAGATCCCAAGAGCTCT 1860
Qy 1861 TGAAGCCCCCGCAGAGGTTTCTCTCCAGCTGGGAGGCTTCGAAACAACCCGAGGCTCC 1920
Db 1861 TGAAGCCCCCGCAGAGGTTTCTCTCCAGCTGGGAGGCTTCGAAACAACCCGAGGCTCC 1920
Qy 1921 TGGGTGCTGAGCAACCTGCGACCGGTGCACTGGTTTGTATATCACTCTAG 1980
Db 1921 TGGGTGCTGAGCAACCTGCGACCGGTGCACTGGTTTGTATATCACTCTAG 1980
Qy 1981 GACCTGTTCTTCTATTTCTGTGTGACTGTTCATTCACAGGATTCATTAACAAAT 2040
Db 1981 GACCTGTTCTTCTATTTCTGTGTGACTGTTCATTCACAGGATTCATTAACAAAT 2040
Qy 2041 TATTGAGTACTTATATCTGCCAGCACCAAGACAAATGATGACAAAGCACTCCTG 2100
Db 2041 TATTGAGTACTTATATCTGCCAGCACCAAGACAAATGATGACAAAGCACTCCTG 2100
Qy 2101 CCTACCTTCGTGAGGTGACAGTTCTCATGAAAGCTGACAGAAATTAATAGCA 2160
Db 2101 CCTACCTTCGTGAGGTGACAGTTCTCATGAAAGCTGACAGAAATTAATAGCA 2160
Qy 2161 GCCAATTTAAACCCAGTGTGAAAGAAAGAAATTAACATCTTGAAGATTTGTCG 2220
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 RESULT 7
 ID AAV51367 standard; DNA; 5300 BP.
 XX AAV51367;
 AC AAV51367;
 XX 27-OCT-1998 (first entry)
 DT 27-OCT-1998 (first entry)
 XX Human TIGR promoter variant TIGRsv1 DNA.
 XX

KM TIGR; trabecular meshwork induced glucocorticoid response protein; human;
 KW diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss..
 XX
 OS Homo sapiens.
 FH Synthetic.
 Key Location/Qualifiers
 FT mutation 4406
 FT /tag= a
 FT /note= "Wild-type A is replaced by G"
 XX
 PN W09832650-A1.
 PD 30-JUL-1998.
 XX
 PF 09-JAN-1998; 98MO-US000468.
 XX
 PR 28-JAN-1997; 97US-00791154.
 PR 26-SEP-1997; 97US-00938669.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PI Nguyen TD, Polansky JR, Chen P, Chen H;
 XX WPI; 1998-427946/36.
 XX
 PT Use of TIGR nucleic acid sequences - used for, e.g. developing products
 PT for diagnosis, prognosis and treatment of glaucoma.
 XX
 PS Disclosure; Fig 2; 105BP; English.
 XX
 CC This sequence is a trabecular meshwork induced glucocorticoid response
 CC protein (TIGR) promoter variant, TIGRv1, which is used in a method for
 CC diagnosing glaucoma in a patient. The method involves the detection of
 CC polymorphisms whose presence is predictive of a mutation affecting TIGR
 CC response in the patient and can be diagnostic of glaucoma or steroid
 CC sensitivity. Base substitutions and base additions upstream of and within
 CC TIGR exons can also be used to diagnose glaucoma
 CC
 SQ Sequence 5300 BP; 1481 A; 1152 C; 1236 G; 1431 T; 0 U; 0 Other;
 Query Match 99.5%; Score 5244.8; DB 2; Length 5300;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 5268; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 421 TAATTAAGATTGTTCTCTGGAGAGAGACCTCCATGATGAGCTTGATGAGAAATGGGAA 480
 DB 421 TAATTAAGATTGTTCTCTGGAGAGAGACCTCCATGATGAGCTTGATGAGAAATGGGAA 480
 QY 481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAGTGATTTATTTTAAAAACAGAT 540
 DB 481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAGTGATTTATTTTAAAAACAGAT 540
 QY 541 GGCATCACTCTGGGAGGCAAGTTCAGGAAGGTATGATAGCAAGGACATCAATAC 600
 DB 541 GGCATCACTCTGGGAGGCAAGTTCAGGAAGGTATGATAGCAAGGACATCAATAC 600
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 DB 661 AGTATTAAGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
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 DB 781 GACATGTTAAAGGCAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 QY 841 GGGACCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 DB 841 GGGACCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
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 DB 901 TTGAAGATCATGATTTTAAACATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 960
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Qy 2401 CCGAAGAAAGAAATGAGAGGGAATCTAGTCTTAAAGGAAATCTGAGAGGAGAGAGTGTTC 2460
Db 2401 CCGAAGAAAGAAATGAGAGGGAATCTAGTCTTAAAGGAAATCTGAGAGGAGAGAGTGTTC 2460
Qy 2461 CTCAGAGGAAAGGGGCTTCCAGCTCCAGAGAAATTCAGAGAGTGGGAGCTGCAAGGAG 2520
Db 2461 CTCAGAGGAAAGGGGCTTCCAGCTCCAGAGAAATTCAGAGAGTGGGAGCTGCAAGGAG 2520
Qy 2521 TGGGAGCTGAGGAGGAGGAGGAGTGTGTAAGAGAGAGAGTGAAGAGGCAAGGCTGTA 2580
Db 2521 TGGGAGCTGAGGAGGAGGAGGAGTGTGTAAGAGAGAGAGTGAAGAGGCAAGGCTGTA 2580
Qy 2581 GCTGCCAGATGTTCAAGTGTGTTCAAGGAGCTGGGAGTTTCCGTGCTCTCTGAGC 2640
Db 2581 GCTGCCAGATGTTCAAGTGTGTTCAAGGAGCTGGGAGTTTCCGTGCTCTCTGAGC 2640

Db 2581 GCTGCCAGATGTTCAAGTGTGTTCAAGGAGCTGGGAGTTTCCGTGCTCTCTGAGC 2640
Qy 2641 CTTTATATCTTCTCTGCTGAGAGAGAGTCTATTTCAAGAGGATGAGTTTC 2700
Db 2641 CTTTATATCTTCTCTGCTGAGAGAGAGTCTATTTCAAGAGGATGAGTTTC 2700
Qy 2701 ATAAAGTCAAGCTGTTAAATTCAGAGGCTGATGAGGTTTCTTCAAGAGCCTTTAT 2760
Db 2701 ATAAAGTCAAGCTGTTAAATTCAGAGGCTGATGAGGTTTCTTCAAGAGCCTTTAT 2760
Qy 2761 TTAATGGGAATATAGGAAGGAGCTCATTTCTGAGGCTGTAATTCACGGAAGAGTGC 2820
Db 2761 TTAATGGGAATATAGGAAGGAGCTCATTTCTGAGGCTGTAATTCACGGAAGAGTGC 2820
Qy 2821 TGAAGCTTTTCTTTCATGCTTTCGAGCACTACTAGCCTGTGTGTAAGTGTGCTTA 2880
Db 2821 TGAAGCTTTTCTTTCATGCTTTCGAGCACTACTAGCCTGTGTGTAAGTGTGCTTA 2880
Qy 2881 TGCAAGAGGTCGAAAGCTTGGAATCAGAGAGACTGGTTTCTTCTGTGTGTGCTAT 2940
Db 2881 TGCAAGAGGTCGAAAGCTTGGAATCAGAGAGACTGGTTTCTTCTGTGTGTGCTAT 2940
Qy 2941 GGTGCTGTGCGAGCCGTGGCAAGTCTCTCTTCCCTGGGCAATAGTCTTCTGCT 3000
Db 2941 GGTGCTGTGCGAGCCGTGGCAAGTCTCTCTTCCCTGGGCAATAGTCTTCTGCT 3000
Qy 3001 ATAAAGACCTTTCAGAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3060
Db 3001 ATAAAGACCTTTCAGAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3060
Qy 3061 GATGCTTGAAGGGGAAAGAGAGAGAGTGTGAGAGCTGTGAGAGCTGTGAGAGAGTGTGAG 3120
Db 3061 GATGCTTGAAGGGGAAAGAGAGAGAGTGTGAGAGCTGTGAGAGCTGTGAGAGAGTGTGAG 3120
Qy 3121 GAGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3180
Db 3121 GAGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3180
Qy 3181 CAGAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3240
Db 3181 CAGAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3240
Qy 3241 TCCCTAAGCATAGACATGAGCTTTGCAATACCAAAAAGATGAGAGATTAAGTCT 3300
Db 3241 TCCCTAAGCATAGACATGAGCTTTGCAATACCAAAAAGATGAGAGATTAAGTCT 3300
Qy 3301 GGTAGCTTTTCCCTGAGATTTCAAAAAGTGGGCGAGAGCAAGTGTGAGAGATTTG 3360
Db 3301 GGTAGCTTTTCCCTGAGATTTCAAAAAGTGGGCGAGAGCAAGTGTGAGAGATTTG 3360
Qy 3361 TTAACCTTTTCAAGCTGAGACCCAGAGCTCAGAGTGTGAGAGTGTGAGAGTGTGAG 3420
Db 3361 TTAACCTTTTCAAGCTGAGACCCAGAGCTCAGAGTGTGAGAGTGTGAGAGTGTGAG 3420
Qy 3421 AGTACCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3480
Db 3421 AGTACCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3480
Qy 3481 ACAGATCATTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3540
Db 3481 ACAGATCATTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3540
Qy 3541 GTTCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3600
Db 3541 GTTCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3600
Qy 3601 CCGATTTCTTAATCAATATTTTCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCT 3660
Db 3601 CCGATTTCTTAATCAATATTTTCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCT 3660
Qy 3661 GTAGTAACTGAGGCTGTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3720
Db 3661 GTAGTAACTGAGGCTGTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3720
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OY	3732	GGAGTTAGCGACAAAGGGCAATCCCGTTCTTTTAA	CAGAAAGAAA	CATTCTTAAGG	3738
Db	3721	GGAGTTAGCGACAAAGGGCAATCCCGTTCTTTTAA	CAGAAAGAAA	CATTCTTAAGG	3726
OY	3781	TAAAGCCAAACGATCAACGCTAGGCTTCTGACTA	TATGATGGTTTTTGA	AAAT	3840
Db	3781	TAAAGCCAAACGATCAACGCTAGGCTTCTGACTA	TATGATGGTTTTTGA	AAAT	3840
OY	3841	CATTTCAGGAGATGTTTACTATCTGATTCAGAAAT	TGAGACTAGACCCCTTGGTCAGCG		3900
Db	3841	CATTTCAGGAGATGTTTACTATCTGATTCAGAAAT	TGAGACTAGACCCCTTGGTCAGCG		3900
OY	3901	TAAACCAACCCGAGTTGTAAATGCTCAAGTTCA	GCTTAACTGCAAGAACCAATCAA		3955
Db	3901	TAAACCAACCCGAGTTGTAAATGCTCAAGTTCA	GCTTAACTGCAAGAACCAATCAA		3960
OY	3960	AAGATFAGATCTTTAGAGCAACATGCTTTCTC	CACATCGGAGGTGATCGCAGGG		4019
Db	3961	AAGATFAGATCTTTAGAGCAACATGCTTTCTC	CACATCGGAGGTGATCGCAGGG		4019
OY	4020	CAGTTTGGAAATTTACTCTCAAGATATGACACT	GCTGTGGTATTAACAACATTAAG		4079
Db	4020	CAGTTTGGAAATTTACTCTCAAGATATGACACT	GCTGTGGTATTAACAACATTAAG		4079
OY	4080	TTCCTCAAGGCATATATTTCAAGGCGTTAAAG	TACTCTGACAGTTTGGTATA		4133
Db	4080	TTCCTCAAGGCATATATTTCAAGGCGTTAAAG	TACTCTGACAGTTTGGTATA		4133
OY	4140	TTTATTTGCTATTTGCCATTTGCTTTTGT	TTTCTCTTTGGTTATTATGTAAAGCA		4199
Db	4140	TTTATTTGCTATTTGCCATTTGCTTTTGT	TTTCTCTTTGGTTATTATGTAAAGCA		4199
OY	4200	GGGATTTATTAACCTACAGTCCAGAAAGCCT	GATGTAATGAGAAAAATTTACATT		4255
Db	4200	GGGATTTATTAACCTACAGTCCAGAAAGCCT	GATGTAATGAGAAAAATTTACATT		4255
OY	4260	TTGTTTTTACCACTTCTTACATTAATTTAA	CAATTTTATTCANTGGCAATTAAGCCATTA		4319
Db	4260	TTGTTTTTACCACTTCTTACATTAATTTAA	CAATTTTATTCANTGGCAATTAAGCCATTA		4319
OY	4320	ACTCAAGAGGTAAATACAGTACCTGATTTT	GTACATACCAATGAATACAGACAT		4379
Db	4320	ACTCAAGAGGTAAATACAGTACCTGATTTT	GTACATACCAATGAATACAGACAT		4379
OY	4380	TTTATCTATATTAACGTTTGGCAGATAGCT	GTGAAGTGAATATTTATCTCAAACT		4439
Db	4380	TTTATCTATATTAACGTTTGGCAGATAGCT	GTGAAGTGAATATTTATCTCAAACT		4439
OY	4440	ACTTTAAATTAAGACCTCCTCGTGATTTT	TTTAACTAATTAATAAACAATCTTTAA		4499
Db	4440	ACTTTAAATTAAGACCTCCTCGTGATTTT	TTTAACTAATTAATAAACAATCTTTAA		4499
OY	4500	AATTTTGAATTTTGAATACTAATTTCAATTA	CAATTTGTTCTTGGTAATCTATATT		4559
Db	4500	AATTTTGAATTTTGAATACTAATTTCAATTA	CAATTTGTTCTTGGTAATCTATATT		4559
OY	4560	TATATATTTGAAAAACATCTTCTGAGAAAG	TAATCCCAAGATTCACCAATGAGGTTCTTG		4619
Db	4560	TATATATTTGAAAAACATCTTCTGAGAAAG	TAATCCCAAGATTCACCAATGAGGTTCTTG		4619
OY	4620	GCATGACACACACAGATTAAGAACTGATTT	TAAGAGGTAACTTGAACATTTGGTGCTGAG		4679
Db	4620	GCATGACACACACAGATTAAGAACTGATTT	TAAGAGGTAACTTGAACATTTGGTGCTGAG		4679
OY	4680	ATGCAAGACTGAATTAAGAACTTCCCAAGAT	TACACAGTTGTTTAAAGCTAGGGAT		4739
Db	4680	ATGCAAGACTGAATTAAGAACTTCCCAAGAT	TACACAGTTGTTTAAAGCTAGGGAT		4739
OY	4740	GAGGGGGGAAATATGCGCTCTTAAGAAATG	CTCTCCGAGAGCTGGATAGGGTGCTGT		4799
Db	4740	GAGGGGGGAAATATGCGCTCTTAAGAAATG	CTCTCCGAGAGCTGGATAGGGTGCTGT		4799

[illegible]

OY	1981	GACCTGTGGTTCTTAATTTCTGTGTGA	CTCGTTCAATTCACAGGACATTCAGCAATT	2040
Db	1981	GACCTGTGGTTCTTAATTTCTGTGTGA	CTCGTTCAATTCACAGGACATTCAGCAATT	2040
OY	2041	TATTGAGTACTTATATCTGCGACAGAC	CAACAGACAAATATGTGTGCAAAAGCATCTGC	2100
Db	2041	TATTGAGTACTTATATCTGCGACAGAC	CAACAGACAAATATGTGTGCAAAAGCATCTGC	2100
OY	2101	CTTACCTTGTGTGAGGTGACAGTTTCT	CATGAGAGCGTGCAGAAAGAAATTAATATAGCA	2160
Db	2101	CTTACCTTGTGTGAGGTGACAGTTTCT	CATGAGAGCGTGCAGAAAGAAATTAATATAGCA	2160
OY	2161	GCCAACTTAAACCCAGTGTGAAAGAA	AGAAATTAACCACTCTTTGAAAGATTGTGGC	2220
Db	2161	GCCAACTTAAACCCAGTGTGAAAGAA	AGAAATTAACCACTCTTTGAAAGATTGTGGC	2220
OY	2221	AGCATCCCTTAAACAAAGCCACCTCC	TGACGCCCCCTGTGCTTCATCGATCGTATCCCGAGAG	2280
Db	2221	AGCATCCCTTAAACAAAGCCACCTCC	TGACGCCCCCTGTGCTTCATCGATCGTATCCCGAGAG	2280
OY	2281	CCCCCAAGCCCGAGTCTTTCAGAGCT	CTCTTCATATGACACAGCGCTGACGCTGGCT	2340
Db	2281	CCCCCAAGCCCGAGTCTTTCAGAGCT	CTCTTCATATGACACAGCGCTGACGCTGGCT	2340
OY	2341	GCTCGCTTCCCGTGAATCGTCTGTG	CACTTGAAGTGAAGACCTTGTGCTTCAGACT	2400
Db	2341	GCTCGCTTCCCGTGAATCGTCTGTG	CACTTGAAGTGAAGACCTTGTGCTTCAGACT	2400
OY	2401	CCGAAAGGAAATGAGAGGGGAAACT	AGTCTAACGAGAACTCTGAGGGGACATGTGTTT	2460
Db	2401	CCGAAAGGAAATGAGAGGGGAAACT	AGTCTAACGAGAACTCTGAGGGGACATGTGTTT	2460
OY	2461	CTCAGAGGGGAAAGGGGCTCCACGCT	CCAGAGAAATTCACAGAGTGTGGAGATGACAGAG	2520
Db	2461	CTCAGAGGGGAAAGGGGCTCCACGCT	CCAGAGAAATTCACAGAGTGTGGAGATGACAGAG	2520
OY	2521	TGGGACCTGTGGGCTGACCGGCTCT	GAAGGACGGAAGGTAAAGGCGCAAGCTAA	2580
Db	2521	TGGGACCTGTGGGCTGACCGGCTCT	GAAGGACGGAAGGTAAAGGCGCAAGCTAA	2580
OY	2581	GCAGCCAGATGTTCAGTGTGTTGTT	CACGCGGCTGAGATTTCGTTGCTCTGTAGC	2640
Db	2581	GCAGCCAGATGTTCAGTGTGTTGTT	CACGCGGCTGAGATTTCGTTGCTCTGTAGC	2640
OY	2641	CTTTTATCTTTCTCTGCTGTGAGAG	AGAAAGTCTATTCTATGAAGGATGCGAGTTTC	2700
Db	2641	CTTTTATCTTTCTCTGCTGTGAGAG	AGAAAGTCTATTCTATGAAGGATGCGAGTTTC	2700
OY	2701	ATAAAGTCAAGTGTAAATTCAGAGG	GTGTGCATGTGCTTCACAGAGGCTTTAT	2760
Db	2701	ATAAAGTCAAGTGTAAATTCAGAGG	GTGTGCATGTGCTTCACAGAGGCTTTAT	2760
OY	2761	TTTATGGGAATATAGGAACGAGCTCA	TTTCTTAGGCGCTTAATATACGAGAAAGTAC	2820
Db	2761	TTTATGGGAATATAGGAACGAGCTCA	TTTCTTAGGCGCTTAATATACGAGAAAGTAC	2820
OY	2821	TGAGAGCTTTTCTTCATGCTTTCTG	GGCACTACAGCCCTGTGTGACATTGAGCTTA	2880
Db	2821	TGAGAGCTTTTCTTCATGCTTTCTG	GGCACTACAGCCCTGTGTGACATTGAGCTTA	2880
OY	2881	TGCAGACGGTGGAAAACCTTGGAA	TACAGAGACTCGGTTTCTTTCTGCTTCCCAAT	2940
Db	2881	TGCAGACGGTGGAAAACCTTGGAA	TACAGAGACTCGGTTTCTTTCTGCTTCCCAAT	2940
OY	2941	GGTTGGCTGTGCAACCGTGGCAATG	TGCTCTCTTCCCTTGAGGCAATGCTTCTCTCT	3000
Db	2941	GGTTGGCTGTGCAACCGTGGCAATG	TGCTCTCTTCCCTTGAGGCAATGCTTCTCTCT	3000
OY	3001	ATAAAGCCCTTGACGCTCTGCTGTT	CTGTGAGACATTCCTGTGTGATCTCTGTGAGGG	3060
Db	3001	ATAAAGCCCTTGACGCTCTGCTGTT	CTGTGAGACATTCCTGTGTGATCTCTGTGAGGG	3060

QY	3061	GGATGTTGAGAGGGGAAAGAGAGCAAGCTGAGAGAGCTGAGCCACAGGGGAGTGTGAGAGG	3120
Dp	3061	GGATGTTGAGAGGGGAAAGAGAGCAAGCTGAGAGAGCTGAGCCACAGGGGAGTGTGAGAGG	3120
QY	3121	GGACAGGAAGGCAAGGCACAAAGCTGGGGTCTCCATCACTCTCTCACTGATATAGCTCAGACTC	3180
Dp	3121	GGACAGGAAGGCAAGGCACAAAGCTGGGGTCTCCATCACTCTCTCACTGATATAGCTCAGACTC	3180
QY	3181	CAGAGCCGAGAGCCCAATGCTTCAGAGAAAGCTCAATGAAACCCACAGCCACATTTTCT	3240
Dp	3181	CAGAGCCGAGAGCCCAATGCTTCAGAGAAAGCTCAATGAAACCCACAGCCACATTTTCT	3240
QY	3241	TCCTTAAGCATGACATATGGCATTTGGCCAAATAACCAAAAAGAAATGACAGACTAACTGGT	3300
Dp	3241	TCCTTAAGCATGACATATGGCATTTGGCCAAATAACCAAAAAGAAATGACAGACTAACTGGT	3300
QY	3301	GGTAGCTTTGGCTGGCATTCAAAACCTGGGGCCAGAGCAAGTGAAGAAATGCCAGAGATTG	3360
Dp	3301	GGTAGCTTTGGCTGGCATTCAAAACCTGGGGCCAGAGCAAGTGAAGAAATGCCAGAGATTG	3360
QY	3361	TTTAACTTTTTCACCTTGACACAGACCCCAAGCAGCTCAGACAGTGTGTGACAGACAGG	3420
Dp	3361	TTTAACTTTTTCACCTTGACACAGACCCCAAGCAGCTCAGACAGTGTGTGACAGACAGG	3420
QY	3421	AGTGAAGCTGACAGCGAGGGGAGAGAAAGAAAGAGAGGAGTATGTTATGACCAAGAG	3480
Dp	3421	AGTGAAGCTGACAGCGAGGGGAGAGAAAGAAAGAGAGGAGTATGTTATGACCAAGAG	3480
QY	3481	ACAGATTCTTCAAGGCGATGGGGAATTGACCCACAGGATTTATGTCACGTAACCTGG	3540
Dp	3481	ACAGATTCTTCAAGGCGATGGGGAATTGACCCACAGGATTTATGTCACGTAACCTGG	3540
QY	3541	GTTCTAGAGGAGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAATCCGGAGA	3600
Dp	3541	GTTCTAGAGGAGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAATCCGGAGA	3600
QY	3601	CCGATTTCTATACTATATTTTCCCTTCAAGCTGAGTAATTCGACAGCAAGTACAG	3660
Dp	3601	CCGATTTCTATACTATATTTTCCCTTCAAGCTGAGTAATTCGACAGCAAGTACAG	3660
QY	3661	GTATTAAGTGAAGGCTGTAAAGTTACTTAGTTTCTCTTATTAAGAACTTTTCTGT	3720
Dp	3661	GTATTAAGTGAAGGCTGTAAAGTTACTTAGTTTCTCTTATTAAGAACTTTTCTGT	3720
QY	3721	GGATTTAGAGACAAAGGGCAATCCGCTTCTTTAAACGAGAAAGAAATATCCCTAAG	3780
Dp	3721	GGATTTAGAGACAAAGGGCAATCCGCTTCTTTTAAACGAGAAAGAAATATCCCTAAG	3780
QY	3781	TAAAGCCAAACAGATTCAAGCTTAGCTTGTCTGACTATATGATGGTTTTTGAAGAAAT	3840
Dp	3781	TAAAGCCAAACAGATTCAAGCTTAGCTTGTCTGACTATATGATGGTTTTTGAAGAAAT	3840
QY	3841	CATTTCAGAGAGTTTATATCTGATTCAGAAAATGACTAGTATACCCCTGGTGTACGCTG	3900
Dp	3841	CATTTCAGAGAGTTTATATCTGATTCAGAAAATGACTAGTATATACCCCTGGTGTACGCTG	3900
QY	3901	TAAACCAACCCACAGTTCTAATGTCTCAAGTTCAAGCTTAACTGCAGAACCAATCAAA-	3959.9
Dp	3901	TAAACCAACCCACAGTTCTAATGTCTCAAGTTCAAGCTTAACTGCAGAACCAATCAAA-	3960
QY	3960	AAAGATAGATCTTTAGAGCAATGTGTTTCCACATCTGAGAGTGAGTCCGACAGG	4019.9
Dp	3961	AAAGATAGATCTTTAGAGCAATGTGTTTCTCCAC-TCGTGAGGTGAGTCTGCACAGG	4019.9
QY	4020	CAGTTTGGAAATTTTACTTCACAGATTTGACAGCTGTGTTGGTATTAACAACATAAG	4079.9
Dp	4020	CAGTTTGGAAATTTTACTTCACAGATTTGACAGCTGTGTTGGTATTAACAACATAAG	4079.9
QY	4080	TTGGTCAAGAGCAATATTTCAAGTGGCTTAAAGTTACTTCTGACAGCTTTGGTATA	4139
Dp	4080	TTGGTCAAGAGCAATATTTTCAAGTGGCTTAAAGTTACTTCTGACAGCTTTGGTATA	4139
QY	4140	TTTATTTGGCTATGCCATTTGCTTTTGTGTTTCTCTTGGGTTATTAATGTAAGCA	4199

D	b	4140	TTTATTGGCTATTGGCATTGGCTTTTGTCTTTTCTCTTGGGTTATTAAATGTAACCA	4199
Q	y	4200	GGGATTATTAACTCAAGTCACAAAAGCCTGTGAAATTGAAATGAGAAAAATTACATT	4259
D	b	4200	GGGATTATTAACTCAAGTCACAAAAGCCTGTGAAATTGAAATGAGAAAAATTACATT	4259
Q	y	4260	TTGTTTTCACACCTTCACATAAATTAAAGTTTATTCATTGCGAATAGACCATTA	4319
D	b	4260	TTGTTTTCACACCTTCACATAAATTATTCATTGCGAATAGACCATTA	4319
Q	y	4320	ACTCAAGTGTGAATPAACAGTACCTGTGATTTTGTCAATTAACAATAGAAATCAGACAT	4379
D	b	4320	ACTCAAGTGTGAATPAACAGTACCTGTGATTTTGTCAATTAACAATAGAAATCAGACAT	4379
Q	y	4380	TTTATACTATATTACAGTTGTGGAGATACGTTGAAGTGAATTTATACATACT	4439
D	b	4380	TTTATACTATATTACAGTTGTGGAGATACGTTGAAGTGAATTTATACATACT	4439
Q	y	4440	ACTTGAATAATAGACCTCTCGTGTGATCTGTGTTTAACTATTAATATTAACATGTTAA	4499
D	b	4440	ACTTGAATAATAGACCTCTCGTGTGATCTGTGTTTAACTATTAATATTAACATGTTAA	4499
Q	y	4500	AATTTTGATATTTTATATATCATATTTCAATATCATTTGTTCCTTGTAATCTAATTT	4559
D	b	4500	AATTTTGATATTTTATATATCATATTTCAATATCATTTGTTCCTTGTAATCTAATTT	4559
Q	y	4560	TATATATTGAAAAACATCTTCTCTGAGAGAGTCCCAAGATTACCAATGAGGTCCTG	4619
D	b	4560	TATATATTGAAAAACATCTTCTCTGAGAGAGTCCCAAGATTACCAATGAGGTCCTG	4619
Q	y	4620	GCATGCACACACAGAGTAAAGAACTGATTAGAGGCTAACATTTGACATTTGGTCTGAG	4679
D	b	4620	GCATGCACACACAGAGTAAAGAACTGATTAGAGGCTAACATTTGACATTTGGTCTGAG	4679
Q	y	4680	ATGCAAGCTGAATTTAGAAAGTTCTCCCAAGATACAGAGTTGTTTAAAGTAGAGGGT	4739
D	b	4680	ATGCAAGCTGAATTTAGAAAGTTCTCCCAAGATACAGAGTTGTTTAAAGTAGAGGGT	4739
Q	y	4740	GAGGGGGGAAATCTGCCGCTTCTATAGAAATGCTCTCCTGAGCCTGTAGAGGTCTGT	4799
D	b	4740	GAGGGGGGAAATCTGCCGCTTCTATAGAAATGCTCTCCTGAGCCTGTAGAGGTCTGT	4799
Q	y	4800	CCTGTGTTCTGGGCTGGCTGTATTCTTCTGTGCTCTGCTAAGTCTTTAAAGCATTTGT	4859
D	b	4800	CCTGTGTTCTGGGCTGGCTGTATTCTTCTGTGCTCTGCTAAGTCTTTAAAGCATTTGT	4859
Q	y	4860	TGGATCTTCAGTTCCTAGCATAGTACCTGCGACAGTSCAGATTCCTCAATAGTTTCAGA	4919
D	b	4860	TGGATCTTCAGTTCCTAGCATAGTACCTGCGACAGTSCAGATTCCTCAATAGTTTCAGA	4919
Q	y	4920	GTGAATGGAATATTAACCTAGAAATATATCTCTGTTGAAATCAGCACACCATGATCTGT	4979
D	b	4920	GTGAATGGAATATTAACCTAGAAATATATCTCTGTTGAAATCAGCACACCATGATCTGT	4979
Q	y	4980	GTGAATGAGTGTGACAGT	5039
D	b	4980	GTGAATGAGTGTGACAGT	5039
Q	y	5040	ATAGAACTATTAATTGGGATGAGGCTGACATAAATGAGATGTTCTTTTAAAGAAACT	5099
D	b	5040	ATAGAACTATTAATTGGGATGAGGCTGACATAAATGAGATGTTCTTTTAAAGAAACT	5099
Q	y	5100	CCAAAGACATCTCGAAGGTTATTTTCTTAAGAAATCTGTGCTGGCAGCGTGAAGCAACC	5159
D	b	5100	CCAAAGACATCTCGAAGGTTATTTTCTTAAGAAATCTGTGCTGGCAGCGTGAAGCAACC	5159
Q	y	5160	CCCTGTGACAGCCCAACCCAGCCTACAGTGGCACATCTGTCTTCCCTCAATGAAGGCT	5219
D	b	5160	CCCTGTGACAGCCCAACCCAGCCTACAGTGGCACATCTGTCTTCCCTCAATGAAGGCT	5219
Q	y	5220	GGCTCCCACTATATATAAATCTCTCTGAGGCTCGGCAATGACCAAGCAAGG	5271

[illegible]

Qy 241 CATCAACAGAGCTAAGAAACAGAAATGATGGCACTTGCCCAAGAAATATGCCAG 300
Db 241 CATCAACAGAGCTAAGAAACAGAAATGATGGCACTTGCCCAAGAAATATGCCAG 300
Qy 301 GAGAGCAATATATGATGAAAAATTAATCTTTCCTTGTGTTTAAATTTTCAGGAAAAATG 360
Db 301 GAGAGCAATATATGATGAAAAATTAATCTTTCCTTGTGTTTAAATTTTCAGGAAAAATG 360
Qy 361 ATAGAGCAACAAATCAATGATGAAAAACAGCTCAGAAAAAGATGTTTCCAAATTGG 420
Db 361 ATAGAGCAACAAATCAATGATGAAAAACAGCTCAGAAAAAGATGTTTCCAAATTGG 420
Qy 421 TAATTAAGTATTTGTTCTTGAGGAAAGACCTCCAGATGAGCTGATGAGGAAAAATGGGA 480
Db 421 TAATTAAGTATTTGTTCTTGAGGAAAGACCTCCAGATGAGCTGATGAGGAAAAATGGGA 480
Qy 481 AAAGCTCAAAAGCATGATCTGATCAGATCCCAAGTGAATTAATTTTAAAAACAGAT 540
Db 481 AAAGCTCAAAAGCATGATCTGATCAGATCCCAAGTGAATTAATTTTAAAAACAGAT 540
Qy 541 GGCATCACTCTGGGAGGCAAGTTCAAGAAAGTCATGTTAGCAAGAGATATCAATTAAC 600
Db 541 GGCATCACTCTGGGAGGCAAGTTCAAGAAAGTCATGTTAGCAAGAGATATCAATTAAC 600
Qy 601 AGCAAAATCAAAATTCGCAAAATGCAAGAAATGGGGAATGGGAAAGCTTTCAATAAC 660
Db 601 AGCAAAATCAAAATTCGCAAAATGCAAGAAATGGGGAATGGGAAAGCTTTCAATAAC 660
Qy 661 AGTATTAGSCAGTGAATGATGTTGCAACACCTCCGCTTATACAGAGAAACAAAA 720
Db 661 AGTATTAGSCAGTGAATGATGTTGCAACACCTCCGCTTATACAGAGAAACAAAA 720
Qy 721 ATTACTGGGCTAAGCCTGACCTTCAAGGAAATATGAAAAATCTAGAGCAAAACAAA 780
Db 721 ATTACTGGGCTAAGCCTGACCTTCAAGGAAATATGAAAAATCTAGAGCAAAACAAA 780
Qy 781 GACATGTTAAAAAGGCAACCAAGAAATGTCAGCTTCAAGAGCAAGTCCCTCAGCA 840
Db 781 GACATGTTAAAAAGGCAACCAAGAAATGTCAGCTTCAAGAGCAAGTCCCTCAGCA 840
Qy 841 GGGACCTGAGGCAATGTCCTTTAGAGAGGCAAGTTTCTTAAGAAATCTTAAGAACTC 900
Db 841 GGGACCTGAGGCAATGTCCTTTAGAGAGGCAAGTTTCTTAAGAAATCTTAAGAACTC 900
Qy 901 TTGAAAGATCATGATTTTAACCATTTTAAGTAAATCAAAATATGCAATGATATGAG 960
Db 901 TTGAAAGATCATGATTTTAACCATTTTAAGTAAATCAAAATATGCAATGATATGAG 960
Qy 961 TTTAGACATGGTCCCAATTTTAAAGTCAAGGCAATCAAGATTAAGTGTCCAGCTCC 1020
Db 961 TTTAGACATGGTCCCAATTTTAAAGTCAAGGCAATCAAGATTAAGTGTCCAGCTCC 1020
Qy 1021 GGAATGGTCAAGAAATCACTTGAATCACTGTGTCCCATCTTAATCTTTTCGAATGATC 1080
Db 1021 GGAATGGTCAAGAAATCACTTGAATCACTGTGTCCCATCTTAATCTTTTCGAATGATC 1080
Qy 1081 TGTCAATAGCCCTCAACACAGAGGCCCAATGTGTCTGAACCTACCAACATCTCAACCCAA 1140
Db 1081 TGTCAATAGCCCTCAACACAGAGGCCCAATGTGTCTGAACCTACCAACATCTCAACCCAA 1140
Qy 1141 GTGCTCAACCATTTGTTAAAGTGTCAATCTCAATAGTCCCATTAAGCAACCTCCCC 1200
Db 1141 GTGCTCAACCATTTGTTAAAGTGTCAATCTCAATAGTCCCATTAAGCAACCTCCCC 1200
Qy 1201 TGTGAGCCCATCCCGCTCCACAGGAAGTCTCCCACTTAAGCTTCTGAGATCAAGATGT 1260
Db 1201 TGTGAGCCCATCCCGCTCCACAGGAAGTCTCCCACTTAAGCTTCTGAGATCAAGATGT 1260
Qy 1261 TACAGCCGAAGGCTCCGTGAAGGCTGAGGCTGTGTCTTACACCTACCTGTATGCTTAC 1320
Db 1261 TACAGCCGAAGGCTCCGTGAAGGCTGAGGCTGTGTCTTACACCTACCTGTATGCTTAC 1320

Qy 1321 ACCTGAGCTCAGTGCACACCTCTGCTCCAGGTTCAAGAAATTCCTGTCTCAGCCTCC 1380
Db 1321 ACCTGAGCTCAGTGCACACCTCTGCTCCAGGTTCAAGAAATTCCTGTCTCAGCCTCC 1380
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Db 1381 CGCGTAGCTGGGACCTACAGAGCGCAGCGCCGCTAATTTTGTATTTAGTATGAGATGGG 1440
Qy 1441 GTTTCACCATATTAAGCCCGGCTGTGTGAATCTCTGACCTCAAGGTATCCACCACTCC 1500
Db 1441 GTTTCACCATATTAAGCCCGGCTGTGTGAATCTCTGACCTCAAGGTATCCACCACTCC 1500
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DB 5220 GGCTCCCGAGTATATATAACCTCTGTGAGCTCGGGCATGAGCCAGCAAGG 5271

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PR 28-JAN-1997; 97US-00791154.
PR 26-SEP-1997; 97US-00938669.
XX (REBC ) UNIV CALIFORNIA.
XX
XX Nguyen TD, Polansky JR, Chen P, Chen H,
XX WPI; 1998-427946/36.
XX
XX Use of TIGR nucleic acid sequences - used for, e.g. developing products
XX for diagnosis, prognosis and treatment of glaucoma.
XX
XX Disclosure; Fig 2; 105pp; English.
XX
XX This sequence is a trabecular meshwork induced glucocorticoid response
XX protein (TIGR) promoter mutant, TIGRmt1, which is used in a method for
XX diagnosing glaucoma in a patient. The method involves the detection of
XX polymorphisms whose presence is predictive of a mutation affecting TIGR
XX response in the patient and can be diagnostic of glaucoma or steroid
XX sensitivity. Base substitutions and base additions upstream of and within
XX TIGR exons can also be used to diagnose glaucoma
XX
XX Sequence 5300 BP; 1482 A; 1151 C; 1236 G; 1431 T; 0 U; 0 Other;
XX
XX Query Match 99.5%; Score 5244.8; DB 2; Length 5300;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 5268; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
XX
QY 1 ATCTTGTTCAGTTTACCTCAGGCGCTATATGAATGAATAGATACCAATGGAAG 60
DB 1 ATCTTGTTCAGTTTACCTCAGGCGCTATATGAATGAATAGATACCAATGGAAG 60
QY 61 TCCCTATTAACCTGATAGCCTCCATTCGATGTATGTCTTGGCAGATGATTAAGATCA 120
DB 61 TCCCTATTAACCTGATAGCCTCCATTCGATGTATGTCTTGGCAGATGATTAAGATCA 120
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DB 421 TAATTAAGATTTTGTCTTGGGAGAGACCTTCCATGTGAGCTGTATAGGAAAATGGGA 480
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Db 3541 GTTCTAG 3600
Qy 3601 CCGTATTTCTAAATCTATTTTCTCTTACAGAGAGATTAATTCAGACAGTCTGACAG 3660
Db 3601 CCGTATTTCTAAATCTATTTTCTCTTACAGAGAGATTAATTCAGACAGTCTGACAG 3660
Qy 3661 GTAGTAACTGAG 3720
Db 3661 GTAGTAACTGAG 3720
Qy 3721 GGAATGTTGAG 3780
Db 3721 GGAATGTTGAG 3780
Qy 3781 TAAAGCCAAACAGATTCAGAGCTGAGTCTGATATATGATGATTTTGTGAAAAT 3840
Db 3781 TAAAGCCAAACAGATTCAGAGCTGAGTCTGATATATGATGATTTTGTGAAAAT 3840
Qy 3841 CATTTCAAGAGATTTTCTATCTGATTCAGAAATGAGACTAGTACCTTTGGTCACTG 3900
Db 3841 CATTTCAAGAGATTTTCTATCTGATTCAGAAATGAGACTAGTACCTTTGGTCACTG 3900
Qy 3901 TAAACAAACCCAGTGTAAATGTCTCAAGTTCAGGCTTAATCTGAGAGAACCAATCAAT 3959
Db 3901 TAAACAAACCCAGTGTAAATGTCTCAAGTTCAGGCTTAATCTGAGAGAACCAATCAAT 3959

3960 AAGAAATAGATCTTTAGAGCAAACTGTGTTTCTCCACATCTGAGAGTAGTCTGCCAGG 4019
Db 3961 AAGAAATAGATCTTTAGAGCAAACTGTGTTTCTCCAC - TCTGAGAGTAGTCTGCCAGG 4019
Qy 4020 CAGTTGGAAATATTTACTTCACAGATATGACATGTGTTGGATTAATTAACCACTAAG 4079
Db 4020 CAGTTGGAAATATTTACTTCACAGATATGACATGTGTTGGATTAATTAACCACTAAG 4079
Qy 4080 TTGCTCAAGAGCAATCATTTTCAAGTGGCTTAAGTACTTCAAGTGTGATTA 4139
Db 4080 TTGCTCAAGAGCAATCATTTTCAAGTGGCTTAAGTACTTCAAGTGTGATTA 4139
Qy 4140 TTTATGGCTATTCAGATTTGCTTTTGTGTTTCTCTTGGGTTTATTAATGTAAGCA 4199
Db 4140 TTTATGGCTATTCAGATTTGCTTTTGTGTTTCTCTTGGGTTTATTAATGTAAGCA 4199
Qy 4200 GGGATTAATTAACCTACAGTCCAGAAAGCTGTGATTTGAATGAGAGAAATTAACATTT 4259
Db 4200 GGGATTAATTAACCTACAGTCCAGAAAGCTGTGATTTGAATGAGAGAAATTAACATTT 4259
Qy 4260 TTGTTTATACACCTTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4319
Db 4260 TTGTTTATACACCTTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4319
Qy 4320 ACTCAAGTGTATTAACAGTACCTGTGATTTTGTATTAACCAATTAATTAATTAATTA 4379
Db 4320 ACTCAAGTGTATTAACAGTACCTGTGATTTTGTATTAACCAATTAATTAATTAATTA 4379
Qy 4380 TTTATATCTATTAATTAACAGTGTGAGATACGTTGATGAGAAATTTTATCTCAAACT 4439
Db 4380 TTTATATCTATTAATTAACAGTGTGAGATACGTTGATGAGAAATTTTATCTCAAACT 4439
Qy 4440 ACTTTGAATTAAGACCTCTGCTGATCTGTTTAACTATTAATTAATTAATTAATTA 4499
Db 4440 ACTTTGAATTAAGACCTCTGCTGATCTGTTTAACTATTAATTAATTAATTAATTA 4499
Qy 4500 AATTTGAATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 4559
Db 4500 AATTTGAATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 4559
Qy 4560 TATATATTTGAAAACATCTTTCTGAGAGAGTCCCAAGATTTCAACCAATGAGTTCTTG 4619
Db 4560 TATATATTTGAAAACATCTTTCTGAGAGAGTCCCAAGATTTCAACCAATGAGTTCTTG 4619
Qy 4620 GCATGACACACACAGATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 4679
Db 4620 GCATGACACACACAGATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAG 4679
Qy 4680 ATCCAAAGACTGAATTAAGAAAGTCTCCCAAGATTAACAGTGTGTTTAAAGCTAGGGGT 4739
Db 4680 ATCCAAAGACTGAATTAAGAAAGTCTCCCAAGATTAACAGTGTGTTTAAAGCTAGGGGT 4739
Qy 4740 GAGGGGGGAAATGTGCGCTTCTATTAAGAAATGCTCTCTGAGAGGCTGTAGGGTGTGT 4799
Db 4740 GAGGGGGGAAATGTGCGCTTCTATTAAGAAATGCTCTCTGAGAGGCTGTAGGGTGTGT 4799
Qy 4800 CTTGTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4859
Db 4800 CTTGTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4859
Qy 4860 TGAATTCAGATTCAGATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGT 4919
Db 4860 TGAATTCAGATTCAGATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGT 4919
Qy 4920 GTGAATGAAATTAATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 4979
Db 4920 GTGAATGAAATTAATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTA 4979
Qy 4980 GTGTAAGTGTGTAGAGT 5039
Db 4980 GTGTAAGTGTGTAGAGT 5039
Qy 5040 ATAGAACTATTTATGGGGATGGGTGATTAATTTGGGATGTCTTTTAAAGAAACT 5099

Db 5040 ATGGAACATATATGAGGTATGGATGATGATTAATGGATGTTCTTTTAAAGAACT 5099
QY 5100 CCAACAGACTTCTGGAAGTTATTTCTTAAGAACTTGTGCGAGCGTGAAGCAACC 5159
Db 5100 CCAACAGACTTCTGGAAGTTATTTCTTAAGAACTTGTGCGAGCGTGAAGCAACC 5159
QY 5160 CCTGTGCAACAGCCCAAGCCCTCAGTGGCCCTCTGTCTTCCCATGAAGGCT 5219
Db 5160 CCTGTGCAACAGCCCAAGCCCTCAGTGGCCCTCTGTCTTCCCATGAAGGCT 5219
QY 5220 GCGTCCCAAGTATATATAACTCTCTGAGAGCTGGGAGATGAGCAAGG 5271
Db 5220 GCGTCCCAAGTATATATAACTCTCTGAGAGCTGGGAGATGAGCAAGG 5271

RESULT 11
AAVS1364
ID AAVS1364 standard; DNA; 5304 BP.

AAVS1364;

27-OCT-1998 (first entry)

Human TIGR promoter mutant TIGRml3 DNA.

TIGR: trabecular meshwork induced glucocorticoid response protein; human;
diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.

Homo sapiens.
Synthetic.

Key Location/Qualifiers
mutation 4997..5002
/tag= a

/note= "Wild-type TG is replaced with TGTGTG"

W09832850-A1.

30-JUL-1998.

09-JAN-1998; 98WC-US000468.

28-JAN-1997; 97US-00791154.

26-SEP-1997; 97US-00938669.

(REGC) UNIV CALIFORNIA.

Nguyen TD, Polansky JR, Chen P, Chen H;

WPI, 1998-427946/36.

Use of TIGR nucleic acid sequences - used for, e.g. developing products
for diagnosis, prognosis and treatment of glaucoma.

Disclosure; Fig 2; 105pp; English.

This sequence is a trabecular meshwork induced glucocorticoid response
protein (TIGR) promoter mutant, TIGRml3, which is used in a method for
diagnosing glaucoma in a patient. The method involves the detection of
polymorphisms whose presence is predictive of a mutation affecting TIGR
response in the patient and can be diagnostic of glaucoma or steroid
sensitivity. Base substitutions and base additions upstream of and within
TIGR exons can also be used to diagnose glaucoma

Sequence 5304 BP; 1482 A; 1152 C; 1237 G; 1433 T; 0 U; 0 Other;

Query Match 99.3%; Score 5232.4; DB 2; Length 5304;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 5269; Conservative 0; Mismatches 1; Indels 6; Gaps 3;

1 ATCTTGTTCAGTTTACCTCAGGCTATATGAATGAATGACATTAACCAATGTGAAG 60
|||||
|||||

Db 1 ATCTTGTTCAGTTTACCTCAGGCTATATGAATGAATGACATTAACCAATGTGAAG 60
QY 61 TCTATTAACCTGTATAGCTTCATTCGATGTATGTCTTTGGCAGATGATTAAGATCA 120
Db 61 TCTATTAACCTGTATAGCTTCATTCGATGTATGTCTTTGGCAGATGATTAAGATCA 120
QY 121 GGAAGAAGATATCCAGTTAGCAGTGTCCAGGCTGTCTGTCTTATTTAGTA 180
Db 121 GGAAGAAGATATCCAGTTAGCAGTGTCCAGGCTGTCTGTCTTATTTAGTA 180
QY 181 CAGATGTTGCTCTGACAGAACTATTCTTCAGAAAATCATCATCOAATATGTAAATC 240
Db 181 CAGATGTTGCTCTGACAGAACTATTCTTCAGAAAATCATCATCOAATATGTAAATC 240
QY 241 CATCAACAGAGCTAAGAAACAGAAATGAGATGGGCACTGCGCAAGAAAAATCCAG 300
Db 241 CATCAACAGAGCTAAGAAACAGAAATGAGATGGGCACTGCGCAAGAAAAATCCAG 300
QY 301 GAGAGCAATATATGATGAAAAATTAACCTTTCCCTTGTGTTTATTTTCAAGAAAAATG 360
Db 301 GAGAGCAATATATGATGAAAAATTAACCTTTCCCTTGTGTTTATTTTCAAGAAAAATG 360
QY 361 ATGAGAACCAATCATGATTAAGAAAAACAGCTCAGAAAAAAGATGTTCCAAATTGG 420
Db 361 ATGAGAACCAATCATGATTAAGAAAAACAGCTCAGAAAAAAGATGTTCCAAATTGG 420
QY 421 TAATTAAGTATTTGTCTTGGAGAGACCTCATGTGAGCTTGAAGGAAAAATGGAA 480
Db 421 TAATTAAGTATTTGTCTTGGAGAGACCTCATGTGAGCTTGAAGGAAAAATGGAA 480
QY 481 AAAGGTCAAAAGCATGATCTGATCAGATCCCAAGTGAATATTTTAAACCAAGAT 540
Db 481 AAAGGTCAAAAGCATGATCTGATCAGATCCCAAGTGAATATTTTAAACCAAGAT 540
QY 541 GGCATCACTCTGGGAGAGCAAGTTCAAGAGTCAATGTTAGCAAGACATTAACATAC 600
Db 541 GGCATCACTCTGGGAGAGCAAGTTCAAGAGTCAATGTTAGCAAGACATTAACATAC 600
QY 601 AGCAAAATCAAAATTCGCAAAATGCAAGAGAAATGCGGACCTGCAAAAGCTTCAATAC 660
Db 601 AGCAAAATCAAAATTCGCAAAATGCAAGAGAAATGCGGACCTGCAAAAGCTTCAATAC 660
QY 661 AGTATTAAGAGAGTGAACATGTTGCAACACTCCCGCTATATACAGAGAAACAAAA 720
Db 661 AGTATTAAGAGAGTGAACATGTTGCAACACTCCCGCTATATACAGAGAAACAAAA 720
QY 721 ATTGACTGGCTTAAGCTGACATTTCAAGGAAATATGAAAACTGAGACAAAAA 780
Db 721 ATTGACTGGCTTAAGCTGACATTTCAAGGAAATATGAAAACTGAGACAAAAA 780
QY 781 GACATGTTTAAAGAGCAACCAATTTGACCTTCAAGAGAGAGAGCCCTCAGCA 840
Db 781 GACATGTTTAAAGAGCAACCAATTTGACCTTCAAGAGAGAGAGCCCTCAGCA 840
QY 841 GGAACCTGAGAGCTTGTGCTTGAAGAGCCAGTTTCTTAAGAACTTAAGAACTC 900
Db 841 GGAACCTGAGAGCTTGTGCTTGAAGAGCCAGTTTCTTAAGAACTTAAGAACTC 900
QY 901 TTGAAGATCATGATTTTAAACATTTTAAGTAAACCAATATCCATCATATCAG 960
Db 901 TTGAAGATCATGATTTTAAACATTTTAAGTAAACCAATATCCATCATATCAG 960
QY 961 TTGAAGATGAGGTCCTCAATTTTAAAGCAGGATCAAGATTAAGTGTCCAGCTC 1020
Db 961 TTGAAGATGAGGTCCTCAATTTTAAAGCAGGATCAAGATTAAGTGTCCAGCTC 1020
QY 1021 GGATAGGTCAAAATCATTAAGAAATCATGTGTCCCATCTTAATTTTCAAGATATC 1080
Db 1021 GGATAGGTCAAAATCATTAAGAAATCATGTGTGTCCCATCTTAATTTTCAAGATATC 1080
QY 1081 TGTATAGCTCTCAACAGAGCCGATGTGTCTGACCTTAACCAACATCTCAACCCCA 1140
Db 1081 TGTATAGCTCTCAACAGAGCCGATGTGTCTGACCTTAACCAACATCTCAACCCCA 1140

OY 1141 GTGCTCAACCATTTGTTAAGTGTCACTCAGTAGGTGCCATTACAAATGCGACCTCCCC 1200
Db 1141 GTGCTCAACCATTTGTTAAGTGTCACTCAGTAGGTGCCATTACAAATGCGACCTCCCC 1200
OY 1201 TGTGCAAGCCATCCCCGTCCACAGGAAGTCTCCCCACTCAAGCTTCTGATCAGATGT 1260
Db 1201 TGTGCAAGCCATCCCCGTCCACAGGAAGTCTCCCCACTCAAGCTTCTGATCAGATGT 1260
OY 1261 TAGAGCCAGAAGCTCCGTGAGGGGTGAGGGTCTGTGCTTACACCTCACTGTATGCTTAC 1320
Db 1261 TAGAGCCAGAAGCTCCGTGAGGGGTGAGGGTCTGTGCTTACACCTCACTGTATGCTTAC 1320
OY 1321 ACCTGAGCTCACTGCAACCTCTGCTCCAGTTCAAGCAATTTCTCTGTCTTCAGCTTCC 1380
Db 1321 ACCTGAGCTCACTGCAACCTCTGCTCCAGTTCAAGCAATTTCTCTGTCTTCAGCTTCC 1380
OY 1381 CGCGTAGCTGGAGCTACAGGGGCAAGCCCGGCTAATTTTGTATGTTGTGTAGAGTGGG 1440
Db 1381 CGCGTAGCTGGAGCTACAGGGGCAAGCCCGGCTAATTTTGTATGTTGTGTAGAGTGGG 1440
OY 1441 GTTTCACCATATTAGCCCGGCTGCTTGTGAATCTCTGACCTCAAGTATCCACCACTTC 1500
Db 1441 GTTTCACCATATTAGCCCGGCTGCTTGTGAATCTCTGACCTCAAGTATCCACCACTTC 1500
OY 1501 AGCCTCTTAAAGTCTGGATTAACAGGCAATGATCAAGCCGCGCCCAAGGTCAGTGT 1560
Db 1501 AGCCTCTTAAAGTCTGGATTAACAGGCAATGATCAAGCCGCGCCCAAGGTCAGTGT 1560
OY 1561 TTAATAAGGAATTAAGTGTGTTACTTAAACCAACAGGGAACAGACAAAGCTGTGA 1620
Db 1561 TTAATAAGGAATTAAGTGTGTTACTTAAACCAACAGGGAACAGACAAAGCTGTGA 1620
OY 1621 TAAATTCAGGGAATCTTGGAGTGGGAATGATGTCATGAGCTGCTGCTTCCAGAC 1680
Db 1621 TAAATTCAGGGAATCTTGGAGTGGGAATGATGTCATGAGCTGCTGCTTCCAGAC 1680
OY 1681 CACGTGCTCATCACTTCTTCCCTCATCTCTCACTTTTCAGGCTAAGTTACATTTAAT 1740
Db 1681 CACGTGCTCATCACTTCTTCCCTCATCTCTCACTTTTCAGGCTAAGTTACATTTAAT 1740
OY 1741 CACCATGCTTTTGTGTATAGGCTTCACATGTTACTGAAATTAAGATATCATTAACATG 1800
Db 1741 CACCATGCTTTTGTGTATAGGCTTCACATGTTACTGAAATTAAGATATCATTAACATG 1800
OY 1801 TTCCATTTGGGGCCATCTGTGTGTGTATAGGGGAGAGGCAATACCCAGAGACTCCT 1860
Db 1801 TTCCATTTGGGGCCATCTGTGTGTGTATAGGGGAGAGGCAATACCCAGAGACTCCT 1860
OY 1861 TGAAGCCCCCGGAGAGGTTCTCTCTCAGCTGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db 1861 TGAAGCCCCCGGAGAGGTTCTCTCTCAGCTGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
OY 1921 TGGGTGCTTGAAGCACTGTCAGACCCGCTGCACTGTTGTTGTATACCTCTCAAG 1980
Db 1921 TGGGTGCTTGAAGCACTGTCAGACCCGCTGCACTGTTGTTGTATACCTCTCAAG 1980
OY 1981 GACCTGTGCTTCTATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
Db 1981 GACCTGTGCTTCTATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
OY 2041 TATGAGTACTTATATCTGCCAGACACCCAGAGCAAAATGTTGAGCAAGCACTCTGC 2100
Db 2041 TATGAGTACTTATATCTGCCAGACACCCAGAGCAAAATGTTGAGCAAGCACTCTGC 2100
OY 2101 CCTACCTTGTGAGAGTACAGTGTCTATGAAAGAGTGTGAGAGAAATTAATAGCA 2160
Db 2101 CCTACCTTGTGAGAGTACAGTGTCTATGAAAGAGTGTGAGAGAAATTAATAGCA 2160
OY 2161 GCCAATTAAACCCAGTGTCTGAAAGAAAGAAATTAACACCATTTGAAAGATTTGTGCG 2220
Db 2161 GCCAATTAAACCCAGTGTCTGAAAGAAAGAAATTAACACCATTTGAAAGATTTGTGCG 2220

OY 2221 AGCATCCCTTAAACAAAGGCCACTTCCCTAGCGCCCTGCTGCTCCTCATGTGTGCGGAG 2280
Db 2221 AGCATCCCTTAAACAAAGGCCACTTCCCTAGCGCCCTGCTGCTCCTCATGTGTGCGGAG 2280
OY 2281 CCCCAGAGCCGAGCTTCCAAAGCTCTCTCTCATCACTCAAGGCTGACAGTGGCT 2340
Db 2281 CCCCAGAGCCGAGCTTCCAAAGCTCTCTCTCATCACTCAAGGCTGACAGTGGCT 2340
OY 2341 GCTGCTTCCGTTGAATGCTCTGTGTGATCTGAGCTGAGACTCTTGGCTCCAGGCT 2400
Db 2341 GCTGCTTCCGTTGAATGCTCTGTGTGATCTGAGCTGAGACTCTTGGCTCCAGGCT 2400
OY 2401 CCAAGAAAGAAATGAGAGGGAACATGATCTAACGGAATCTGAGAGGGAACAGTGTTC 2460
Db 2401 CCAAGAAAGAAATGAGAGGGAACATGATCTAACGGAATCTGAGAGGGAACAGTGTTC 2460
OY 2461 CTCAGAGGAAGAGGCTTCCAGTCCAGAGAAATTCAGAGGTGGGACTGCAAGAG 2520
Db 2461 CTCAGAGGAAGAGGCTTCCAGTCCAGAGAAATTCAGAGGTGGGACTGCAAGAG 2520
OY 2521 TGGGAGAGCTGGGCTGAGCGGCTGTGAAGGCAAGAGAGTGAAGGCAAGCTGTA 2580
Db 2521 TGGGAGAGCTGGGCTGAGCGGCTGTGAAGGCAAGAGAGTGAAGGCAAGCTGTA 2580
OY 2581 GCTGCCAGATGTTCAAGTGTGTTCAAGGGGCTGGAGGTTTCCGTTGCTCTGTAGC 2640
Db 2581 GCTGCCAGATGTTCAAGTGTGTTCAAGGGGCTGGAGGTTTCCGTTGCTCTGTAGC 2640
OY 2641 CTTTATCTTTCTCTGCTGAGAGAAAGATCTAATTCAATGAAGGATGCACTTTC 2700
Db 2641 CTTTATCTTTCTCTGCTGAGAGAAAGATCTAATTCAATGAAGGATGCACTTTC 2700
OY 2701 ATAAAGTCACTGTAAATTCAGAGGTGTGATGAGGTTTCTTCAAGAGGCTTAT 2760
Db 2701 ATAAAGTCACTGTAAATTCAGAGGTGTGATGAGGTTTCTTCAAGAGGCTTAT 2760
OY 2761 TTAATGGAATATAGAAAGCAAGCTCAATTCAGGCGGTTAATTCAGGAAAGATGAC 2820
Db 2761 TTAATGGAATATAGAAAGCAAGCTCAATTCAGGCGGTTAATTCAGGAAAGATGAC 2820
OY 2821 TGAAGTCTTTCTTATATGCTTCTGTGGCAATCACTCAGCCGTGTGTGACTGGCTTA 2880
Db 2821 TGAAGTCTTTCTTATATGCTTCTGTGGCAATCACTCAGCCGTGTGTGACTGGCTTA 2880
OY 2881 TGCAAGACGTCGAAACCTTGAATCAGAGAGCTGATTTCTTCTGCTCTGCAAT 2940
Db 2881 TGCAAGACGTCGAAACCTTGAATCAGAGAGCTGATTTCTTCTGCTCTGCAAT 2940
OY 2941 GGTGCTGTGCAAGCTGTGGCAAGTGTCTCTCTTCCCTGGGCAATGCTTCTCTGCT 3000
Db 2941 GGTGCTGTGCAAGCTGTGGCAAGTGTCTCTCTTCCCTGGGCAATGCTTCTCTGCT 3000
OY 3001 ATAAAGACCTTGAAGTCTGTGCTGTGGAACAATTCCTGCTGATCTGTGAGGG 3060
Db 3001 ATAAAGACCTTGAAGTCTGTGCTGTGGAACAATTCCTGCTGATCTGTGAGGG 3060
OY 3061 GATGTTGAGAGGGGAAGAGGAGAGAGCTGAGACAGTGAAGCCAGAGGAGGTGAGGG 3120
Db 3061 GATGTTGAGAGGGGAAGAGGAGAGAGCTGAGACAGTGAAGCCAGAGGAGGTGAGGG 3120
OY 3121 GGAAGAGAGGCAAGGCAAGCTGTGCTCACTGCTCACTGATCAAGTCAAGTCA 3180
Db 3121 GGAAGAGAGGCAAGGCAAGCTGTGCTCACTGCTCACTGATCAAGTCAAGTCA 3180
OY 3181 CAGAGCCAGAGCCACATGCTTCAAGAAAGCTCAATGAAGCCCAAGCCACATTTCT 3240
Db 3181 CAGAGCCAGAGCCACATGCTTCAAGAAAGCTCAATGAAGCCCAAGCCACATTTCT 3240
OY 3241 TCCCTAAGCATAGCAATGAGATTTGCAATTAACCAAAAGATGAGAGACTAATGTGT 3300
Db 3241 TCCCTAAGCATAGCAATGAGATTTGCAATTAACCAAAAGATGAGAGACTAATGTGT 3300
OY 3301 GTAGACTTTGCTGCAATTCAAAACTGGGCGAGAGCAAGTGAAGAAATGCGAGATTTG 3360

Db	3301	GGTAGCTTTGGCTGGCAATTCAAAACTGGGCGAGACCAAGTGAATAATGCGAGGATTG	3360
Qy	3361	TTAAACTTTTCACTCGACACAGACCCCAACAGCTGAGATGCTGTGACACACAGG	3420
Db	3361	TTAACTTTTCACTCGACACAGACCCCAACAGCTGAGATGCTGTGACACACAGG	3420
Qy	3421	AGTACCTGCAAGCGCGAGGAGAGAGAAAGAAAGAGGCGATGTGTATGACAGAAAG	3480
Db	3421	AGTACCTGCAAGCGCGAGGAGAGAGAAAGAAAGAGGCGATGTGTATGACAGAAAG	3480
Qy	3481	ACAGATCATTCAGAGGGCAGTGGGAATGACCAAGGGAATTATAGTCCAGCTGTCTGG	3540
Db	3481	ACAGATCATTCAGAGGGCAGTGGGAATGACCAAGGGAATTATAGTCCAGCTGTCTGG	3540
Qy	3541	GTTCTAGAGGCGAGGCTATATGTGGGAGGAAAAATCATGTTCAAGGAAAGTCCGAG	3600
Db	3541	GTTCTAGAGGCGAGGCTATATGTGGGAGGAAAAATCATGTTCAAGGAAAGTCCGAG	3600
Qy	3601	CCGATTTCTTAATACATATTTTCTTTTCAAGCTAGTATTTGACACAGTACAG	3660
Db	3601	CCGATTTCTTAATACATATTTTCTTTTCAAGCTAGTATTTGACACAGTACAG	3660
Qy	3661	GTAGTAATCAGGCGGTGTAAGATTACTAGTTCAGTTCCTATTAGAACTCTTTTCTGT	3720
Db	3661	GTAGTAATCAGGCGGTGTAAGATTACTAGTTCAGTTCCTATTAGAACTCTTTTCTGT	3720
Qy	3721	GGAGTTAGACAGCAAGGCGAATCCCGTTCTTTTACAGAGAAATACATCTCTAAG	3780
Db	3721	GGAGTTAGACAGCAAGGCGAATCCCGTTCTTTTACAGAGAAATACATCTCTAAG	3780
Qy	3781	TAAAGCCAAACAGATTCAAGCTAGTCTTGCTGACTATATGATGTGTTTGTGAAAT	3840
Db	3781	TAAAGCCAAACAGATTCAAGCTAGTCTTGCTGACTATATGATGTGTTTGTGAAAT	3840
Qy	3841	CATTTCAGGAGTTTACTATCTATCTGATTAAGAAAATGAGACTAGTACCTTTGGTCACTG	3900
Db	3841	CATTTCAGGAGTTTACTATCTATCTGATTAAGAAAATGAGACTAGTACCTTTGGTCACTG	3900
Qy	3901	TAAACAAACACACAGTGTAAATGCTACAGTTAAGGCTTAAGTGCAGAACCAATCAA-	3959
Db	3901	TAAACAAACACCACTTTGTAAATGCTCAGTTCAAGCTTAAGTGCAGAACCAATCAA	3959
Qy	3960	AAGATAGAACTTTTAGAGCAAACTGTGTCTCCACATCTGAGGTGAGTCTGCAAGG	4019
Db	3961	AAGATAGAACTTTTAGAGCAAACTGTGTCTCCAC-TCGAGGTTGAGTCTGCAAGG	4019
Qy	4020	CAGTTGSAATTAATTAATCTCAAGATTAAGACACGTGTGATTAACAACTAAG	4079
Db	4020	CAGTTGSAATTAATTAATCTCAAGATTAAGACACGTGTGTGATTAACAACTAAG	4079
Qy	4080	TTGCTCAAGAGCAATCATTAATTAAGAGGCTTAAAGTTACTCTGCACAGTTTGTATA	4139
Db	4080	TTGCTCAAGAGCAATCATTAATTAAGAGGCTTAAAGTTACTCTGCACAGTTTGTATA	4139
Qy	4140	TTTATTTGGCTATTGCACTTTGCTTTTGTTTTCTCTTTGGTTTATTAATGTAAGCA	4199
Db	4140	TTTATTTGGCTATTGCACTTTGCTTTTGTTTTCTCTTTGGTTTATTAATGTAAGCA	4199
Qy	4200	GGGATTTATTAACCTACAGTCCAGAGAACTGTGAATTTGATAGAGGAAAAATTAACATTT	4259
Db	4200	GGGATTTATTAACCTACAGTCCAGAGAACTGTGAATTTGATAGAGGAAAAATTAACATTT	4259
Qy	4260	TTGTTTTTCCACCTTCTTAACCTAAATTTAACTTTATTCATTTGCAATGAGCATTA	4319
Db	4260	TTGTTTTTCCACCTTCTTAACCTAAATTTAACTTTATTCATTTGCAATGAGCATTA	4319
Qy	4320	ACTCAAGAGGTAATTAACAGTACCGTGAATTTGTCTTAACCAATGAATACAGCAT	4379
Db	4320	ACTCAAGAGGTAATTAACAGTACCGTGAATTTGTCTTAACCAATGAATACAGCAT	4379
Qy	4380	TTTATCTATATTAACAGTTGTGCAATAGCTGTAAAGAAATTTATATCTCAAACT	4439

[illegible]

QY 1261 TACAGCCAGAGCTCCGTGAGGAGGAGGCTGTGTCTTACACCTAAGCTGTAGCTTAC 1320
Db 1261 TAGAGCCAGAGAGCTCCGTGAGGAGGAGGCTGTGTCTTACACCTAAGCTGTAGCTTAC 1320
QY 1321 ACTGAGCTCACTGCAACCTCTCTCTCCCAAGCTTCAAGCAATTTCTGTCTCAAGCTTC 1380
Db 1321 ACCGAGCTCACTGCAACCTCTCTCTCCCAAGCTTCAAGCAATTTCTGTCTCAAGCTTC 1380
QY 1381 CGAGTAGCTGGAGCTACAGAGCGACGCGGCTAATTTTGTATTTGTATGTAGTGAATGG 1440
Db 1381 CGCGTAGCTGGAGCTACAGAGCGACGCGGCTAATTTTGTATTTGTATGTAGTGAATGG 1440
QY 1441 GTTTCACCAATATTAGCCCGGCTGTGTGAATCTTGAACCTCAGCTCAGGTATCCACCCACTC 1500
Db 1441 GTTTCACCAATATTAGCCCGGCTGTGTGAATCTTGAACCTCAGCTCAGGTATCCACCCACTC 1500
QY 1501 AGGCTCCTAAGAGTCTGAGGATTTACAGGCAATGATCAAGCGGCGCCGCAAGGCTGAGT 1560
Db 1501 AGGCTCCTAAGAGTCTGAGGATTTACAGGCAATGATCAAGCGGCGCCGCAAGGCTGAGT 1560
QY 1561 TTAATAAGGAATACTTGAATGATTTACTTAACCAACAGGGAACAGACAAAGCTGTA 1620
Db 1561 TTAATAAGGAATACTTGAATGATTTACTTAACCAACAGGGAACAGACAAAGCTGTA 1620
QY 1621 TAATTTCAAGGATTTCTTGGATTTGGGAAATGTCCTCAAGCTGCTGCTGCTGCTGCTGAC 1680
Db 1621 TAATTTCAAGGATTTCTTGGATTTGGGAAATGTCCTCAAGCTGCTGCTGCTGCTGCTGAC 1680
QY 1681 CACTGTCTCATCATCTTCTTCCCTCATCTCATCTTTCAGGCTAAGTATACATTTTAT 1740
Db 1681 CACTGTCTCATCATCTTCTTCCCTCATCTCATCTTTCAGGCTAAGTATACATTTTAT 1740
QY 1741 CACCAATGCTTTTGTGTGAATGCTCCACATCGTTACTGAATTAAGATTAACATACTAG 1800
Db 1741 CACCAATGCTTTTGTGTGAATGCTCCACATCGTTACTGAATTAAGATTAACATACTAG 1800
QY 1801 TTCCATTTGGGAGCATCTGTGTGTGTGTATAGGGAGAGAGGCAATCCCGAGACATCCT 1860
Db 1801 TTCCATTTGGGAGCATCTGTGTGTGTGTATAGGGAGAGAGGCAATCCCGAGACATCCT 1860
QY 1861 TGAAGCCCCCGGAGAGGTTTCTCTCCAGCTGGGGAGCCCTGGAACACCCGGGGTCC 1920
Db 1861 TGAAGCCCCCGGAGAGGTTTCTCTCCAGCTGGGGAGCCCTGGAACACCCGGGGTCC 1920
QY 1921 TGGGTCTCTGAGCAACCTGCGACGCGGCTGCACTGTGTGTGTGTATCTCTAGG 1980
Db 1921 TGGGTCTCTGAGCAACCTGCGACGCGGCTGCACTGTGTGTGTATCTCTAGG 1980
QY 1981 GACCTGTCTCTTCTATTTCTGTGTGACTCGTTCAATTCAGGCAATCTTGAACAT 2040
Db 1981 GACCTGTCTCTTCTATTTCTGTGTGACTCGTTCAATTCAGGCAATCTTGAACAT 2040
QY 2041 TATTGAGTACTTATATCTGTGCAAGACACAGACAAATGCTGAGCAAAAGCACTGTC 2100
Db 2041 TATTGAGTACTTATATCTGTGCAAGACACAGACAAATGCTGAGCAAAAGCACTGTC 2100
QY 2101 CCTACCTTGTGAGAGTGAAGTTTCTCATGAGAGAGTGCAGAGAGAAATTAATACCA 2160
Db 2101 CCTACCTTGTGAGAGTGAAGTTTCTCATGAGAGAGTGCAGAGAGAAATTAATACCA 2160
QY 2161 GCCAATTAACCCAGTGTGAGAGAGAGAAATTAACCAATCTTGAAGATTTGTGCGC 2220
Db 2161 GCCAATTAACCCAGTGTGAGAGAGAGAAATTAACCAATCTTGAAGATTTGTGCGC 2220
QY 2221 AGCATTCCTTTAAGAGGCACTCTCTGAGCGGCTCTGTCTCTCATCTGCTGCGGAGG 2280
Db 2221 AGCATTCCTTTAAGAGGCACTCTCTGAGCGGCTCTGTCTCTCATCTGCTGCGGAGG 2280
QY 2281 CCCCCAAGCCGAGTCTTCAAGCTCTCTCTCATCATGATCAAGGCTGAGGCTGAGGCT 2340
Db 2281 CCCCCAAGCCGAGTCTTCAAGCTCTCTCTCATCATGATCAAGGCTGAGGCTGAGGCT 2340
QY 2341 GCGTCGCTTCCGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400

Db 2341 GCGTCGCTTCCGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400
QY 2401 CCAGAAAGGAAATGAGAGAGGAACTAGCTTAACGAGAAATCTGAGAGGCAAGTGTTC 2460
Db 2401 CCAGAAAGGAAATGAGAGAGGAACTAGCTTAACGAGAAATCTGAGAGGCAAGTGTTC 2460
QY 2461 CTCAGAGGAAAGGGGCTCCACGCTCAGAGAAATTCAGAGAGGTTGGGAGCTGAGAGGAG 2520
Db 2461 CTCAGAGGAAAGGGGCTCCACGCTCAGAGAAATTCAGAGAGGTTGGGAGCTGAGAGGAG 2520
QY 2521 TGGGAGCGCTGGGAGTGAAGCGGCTGCTGAAAGGAGAGAGAGGAGGAGGAGGAGGAG 2580
Db 2521 TGGGAGCGCTGGGAGTGAAGCGGCTGCTGAAAGGAGAGAGAGGAGGAGGAGGAGGAG 2580
QY 2581 GCTGCCAAGATTTAGATTTGTTCACGGGAGCTGGAGTTTCCGTGCTTCTGTAGC 2640
Db 2581 GCTGCCAAGATTTAGATTTGTTCACGGGAGCTGGAGTTTCCGTGCTTCTGTAGC 2640
QY 2641 CTTTATATCTTCTCTGCTTGAAGAGAAATTAATTCATGAGAGGATGAGGATTC 2700
Db 2641 CTTTATATCTTCTCTGCTTGAAGAGAAATTAATTCATGAGAGGATGAGGATTC 2700
QY 2701 ATAAAGTCAAGCTTTAAATTCAGAGGCTGATGAGGTTTCTTCAAGAGCTTTAT 2760
Db 2701 ATAAAGTCAAGCTTTAAATTCAGAGGCTGATGAGGTTTCTTCAAGAGCTTTAT 2760
QY 2761 TTAATGGGAATTAAGAGAGGAGCTAATTCAGAGGCTGATGAGGAGGAGGAGGAG 2820
Db 2761 TTAATGGGAATTAAGAGAGGAGCTAATTCAGAGGCTGATGAGGAGGAGGAGGAGGAG 2820
QY 2821 TGAAGTCTTTTCTTCTGATGCTTCTGAGCAATCTAGAGCTGTGTGTGAGCTTGA 2880
Db 2821 TGAAGTCTTTTCTTCTGATGCTTCTGAGCAATCTAGAGCTGTGTGTGAGCTTGA 2880
QY 2881 TGCAGAGAGTGCAGAAACCTTGAATCAGAGAGCTGCTTCTTCTGCTGCTGCTGCT 2940
Db 2881 TGCAGAGAGTGCAGAAACCTTGAATCAGAGAGCTGCTTCTTCTGCTGCTGCTGCTGCT 2940
QY 2941 GGTGAGCTGTGCAAGCTGTGGCAAGTCTCTCTTCTGAGGCAATGCTTCTGCTGCT 3000
Db 2941 GGTGAGCTGTGCAAGCTGTGGCAAGTCTCTCTTCTGAGGCAATGCTTCTGCTGCTGCT 3000
QY 3001 ATAAAGACCTTGTGAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3060
Db 3001 ATAAAGACCTTGTGAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3060
QY 3061 GATGTTGAGAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3120
Db 3061 GATGTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3120
QY 3121 GACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3180
Db 3121 GACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3180
QY 3181 CAGAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3240
Db 3181 CAGAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3240
QY 3241 TCCCTAAGCATTAAGCAATGAGATTTGCAATTAACAAAGATGAGAGATTAAGTGT 3300
Db 3241 TCCCTAAGCATTAAGCAATGAGATTTGCAATTAACAAAGATGAGAGATTAAGTGT 3300
QY 3301 GATGAGCTTTGCTGTGATTTCAAAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3360
Db 3301 GATGAGCTTTGCTGTGATTTCAAAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3360
QY 3361 TTAAGCTTTTCAAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3420
Db 3361 TTAAGCTTTTCAAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3420
QY 3421 AGTGAAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3480

Db 1799 TATATATAAAGCTCTGTGAGCTCGGGCATGAGCCAGCAGG 1840

RESULT 14
ABA96249
ID ABA96249 standard; DNA; 476 BP.
XX
AC ABA96249;
XX
DT 14-MAR-2002 (first entry)
XX
DE Human glaucoma diagnosis related polynucleotide SEQ ID NO 2.
XX
KW Human; diagnosis; glaucoma; ds.
XX
OS Homo sapiens.
XX
EN WO200188120-A1.
XX
PD 22-NOV-2001.
XX
PE 16-MAY-2001; 2001WO-JP004067.
XX
PR 17-MAY-2000; 2000JP-00144492.
XX
PA (TSUB-) TSUBOTA LTD.
PA (HATT) HATTORI Y.
PA (SUZU/) SUZUKI R.
XX
PI Hattori Y, Suzuki R;
XX
DR WPI; 2002-114235/15.
XX
PT Polynucleotides for pre-diagnosis of glaucoma.
XX
PS Claim 2; Page 20; 26pp; Japanese.
XX
CC The invention relates to a polynucleotide (ABA96249) useful for pre-
CC diagnosing glaucoma. The present sequence is that of a glaucoma diagnosis
CC related polynucleotide of the invention
XX
SQ Sequence 476 BP; 123 A; 116 C; 118 G; 119 T; 0 U; 0 Other;
Query Match 7.5%; Score 394.4; DB 6; Length 476;
Best Local Similarity 99.3%; Pred. No. 1.1e-79;
Matches 407; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
QY 4862 GATCTCCAGTTCCTAGCATAGTGTGCTTGGCAGAGTTCGATGAGTTGCGAGT 4921
DB 1 GATCTCCAGTTCCTAGCATAGTGTGCTTGGCAGAGTTCGATGAGTTGCGAGT 60
QY 4922 GAATGGAATATAAAGTAAAGTAAATATCTGTTGAATCAGCAGCAGCAGTCTGCT 4981
DB 61 GAATGGAATATAAAGTAAAGTAAATATCTGTTGAATCAGCAGCAGCAGTCTGCT 120
QY 4982 GTAAGTGTGTAGCTGT 5041
DB 121 GTAAGTGTGTAGCTGT 178
QY 5042 AGGAATCTATTTATGGGGTATGGGTGCAAAATTTGGGATGTTCTTTTAAAAAGAACTCC 5101
DB 179 AGGAATCTATTTATGGGGTATGGGTGCAAAATTTGGGATGTTCTTTTAAAAAGAACTCC 238
QY 5102 AAACAGCTTCTGGAAGGTATTTTCTAAGATCTTCTGCGACCGTGAAGGCAACCCCC 5161
DB 239 AAACAGCTTCTGGAAGGTATTTTCTAAGATCTTCTGCGACCGTGAAGGCAACCCCC 298
QY 5162 CTGTGCAAGCCCAACCAAGCTCAGCGTGGCACTCTGTCTTCCCAATGAAGGGCTGG 5221
DB 299 CTGTGCAAGCCCAACCAAGCTCAGCGTGGCACTCTGTCTTCCCAATGAAGGGCTGG 358
QY 5222 CTCGCCAGTATATATAAAGCTCTGTGAGCTCGGGCATGAGCCAGCAGG 5271

Db 359 CTCGCCAGTATATATAAAGCTCTGTGAGCTCGGGCATGAGCCAGCAGG 408

RESULT 15
ACA64937
ID ACA64937 standard; DNA; 1086 BP.
XX
AC ACA64937;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human GLC1A DNA corresponding to Z97171.
XX
KW Human; chronic inflammatory joint disease; infection; tumour;
KW antiinflammatory; cytosolic; antirheumatic; antirheumatic;
KW immunosuppressive; gene therapy; etiological pathogenicity; ds.
XX
OS Homo sapiens.
XX
EN DE10127572-A1.
XX
PD 05-DEC-2002.
XX
PE 30-MAY-2001; 2001DE-01027572.
XX
PR 30-MAY-2001; 2001DE-01027572.
XX
PA (PATH-) PATHOARRAY GMBH.
XX
PI Haepfl T, Ungethuen U, Blaess S;
XX
DR WPI; 2003-240797/24.
XX
PT Reagents for diagnosis, study and therapy of chronic inflammatory joint
PT and other diseases, comprises any of many specified genes or derived
PT proteins.
XX
PS Claim 1; Page; 12pp; German.
XX
CC This invention describes a novel reagent for diagnosis, molecular
CC definition and therapy of chronic inflammatory joint diseases, and other
CC inflammatory disorders, infective or tumour diseases in humans. The
CC products of the invention have antiinflammatory, cytosolic,
CC antiarthritic, antirheumatic and immunosuppressive activity and can be
CC used for gene therapy. The reagent of the invention and any proteins and
CC antibodies derived from it, are used (i) for analysing tissue and blood
CC samples for medical diagnosis; (ii) for diagnosis and characterisation of
CC chronic joint diseases, on the basis of molecular characterisation, and
CC determining the etiological pathogenicity principle of as yet
CC uncharacterised inflammatory diseases, also monitoring progression and/or
CC treatment of disease, and optimisation of therapy and (iii) for
CC developing treatments for inflammatory diseases, particularly of joints,
CC infections and tumours. ACA64801-ACA64965 represent human polynucleotides
XX
SQ Sequence 1086 BP; 277 A; 282 C; 316 G; 211 T; 0 U; 0 Other;
Query Match 7.5%; Score 394.4; DB 7; Length 1086;
Best Local Similarity 99.7%; Pred. No. 1.0e-79;
Matches 395; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4876 AGCATAGGCTGCGCAGAGTGTCTCAATGAGTTTCAGAGTGAATGAATATTA 4935
DB 1 AGCATAGGCTGCGCAGAGTGTCTCAATGAGTTTCAGAGTGAATGAATATTA 60
QY 4936 ACTAGAAATATATCTTGTGAATTCAGCACACAGTATGCTGTGTAAGTGTGTAC 4995
DB 61 ACTAGAAATATATCTTGTGAATTCAGCACACAGTATGCTGTGTAAGTGTGTAC 120
QY 4996 GTGTCTGT 5055
DB 121 GTGTCTGT 180

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QY 5056 GGGTATGGGTGCAATAATTGGGATGTTCTTTTAAAAAGAACTCCAAACAGACTTCTGG 5115
Db 181 GGGTATGGGTGCAATAATTGGGATGTTCTTTTAAAAAGAACTCCAAACAGACTTCTGG 240
QY 5116 AAGGTATTTTCTAAGAAATCTGCTGGCAGCCGTGAAGGCAACCCCTGTGTACAGCCCC 5175
Db 241 AAGGTATTTTCTAAGAAATCTGCTGGCAGCCGTGAAGGCAACCCCTGTGTACAGCCCC 300
QY 5176 ACCCAGCCTCAGTGGCCACCTCTGTCTTCCCCATGAAGGGCTGCTCCCGATATATA 5235
Db 301 ACCCAGCCTCAGTGGCCACCTCTGTCTTCCCCATGAAGGGCTGCTCCCGATATATA 360
QY 5236 TAAACCTCTCTGAGAGCTCGGGCATGAGCCAGCAAG 5271
Db 361 TAAACCTCTCTGAGAGCTCGGGCATGAGCCAGCAAG 396

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Search completed: September 18, 2004, 21:06:14
 Job time : 1892 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 19, 2004, 12:16:22 / Search time 12228 Seconds
(without alignments)
12872.387 Million cell updates/sec

Title: US-09-227-881-34
Perfect score: 5271
Sequence: 1 atcttgcagttcattcctc.....tcggcagtcagccagcaagg 5271

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: EST:*

1:	em_estba:*
2:	em_estlum:*
3:	em_estlin:*
4:	em_estmu:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_hnc:*
9:	gb_estl:*
10:	gb_est2:*
11:	gb_hnc:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estum:*
16:	em_estom:*
17:	em_gss_hum:*
18:	em_gss_inv:*
19:	em_gss_pln:*
20:	em_gss_vre:*
21:	em_gss_fun:*
22:	em_gss_mam:*
23:	em_gss_mus:*
24:	em_gss_pro:*
25:	em_gss_rtd:*
26:	em_gss_phg:*
27:	em_gss_vrl:*
28:	gb_gest:*
29:	gb_gest2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	186.6	3.5	710	13	BU849843 AGENCOURT
C 2	182.4	3.5	515	14	CA946732 1s09h12.x
C 3	180.8	3.4	660	28	AO057239 CIT-HSP-2
C 4	179.8	3.4	539	28	AO379787 RPII11-15

C 5	179.2	3.4	340	13	BU957861
C 6	179	3.4	597	14	CB268731
C 7	179	3.4	613	28	A2520729 RPII-11-7
C 8	179	3.4	645	28	AO636457 RPII-11-4
C 9	179	3.4	678	28	AO387027 RPII11-15
C 10	178.6	3.4	887	12	BG541228 602570320
C 11	178.4	3.4	537	10	AM978041 EST390150
C 12	177.8	3.4	590	12	BM803650 AGENCOURT
C 13	177.6	3.4	516	28	AQ112451 CIT-HSP-2
C 14	177.4	3.4	577	28	AO265389
C 15	177.2	3.4	548	9	AI583291
C 16	177	3.4	400	10	BF920612
C 17	177	3.4	769	13	BU854207
C 18	176.8	3.4	784	12	BM556091
C 19	176.6	3.4	413	13	EX478124
C 20	176.6	3.4	434	28	AQ159435
C 21	176.6	3.4	573	12	BM990011
C 22	176.6	3.4	591	10	AM979191
C 23	176.4	3.3	501	13	EX646708
C 24	176.4	3.3	568	14	CD517289
C 25	176.2	3.3	494	9	AL698462
C 26	176	3.3	521	10	AM273360
C 27	176	3.3	551	14	TS3829
C 28	175.8	3.3	589	28	AO283440
C 29	175.6	3.3	493	9	AU146498
C 30	175.6	3.3	607	28	BZ603705
C 31	175.4	3.3	386	28	AO474222
C 32	175.4	3.3	593	14	CD329747
C 33	175.2	3.3	393	10	BF905088
C 34	175.2	3.3	548	9	AV711892
C 35	175.2	3.3	662	9	AV701462
C 36	175.2	3.3	670	12	BM671184
C 37	175.2	3.3	711	28	AO415030
C 38	175	3.3	388	9	AM659237
C 39	175	3.3	421	10	AM674631
C 40	175	3.3	447	10	AM820784
C 41	175	3.3	454	9	AI634187
C 42	175	3.3	474	9	AI457313
C 43	175	3.3	527	9	AI523813
C 44	175	3.3	546	12	BM697526
C 45	175	3.3	563	9	AU144540

ALIGNMENTS

RESULT 1
BU849843/c 710 bp mRNA linear EST 16-OCT-2002
AGENCOURT_10440376 NIH_MGC_109 Homo sapiens cDNA clone
IMAGE:6598537 5', mRNA sequence.

ACCESSION BU849843
VERSION BU849843.1 GI:24034806
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
1 (bases 1 to 710)
TITLE: Unpublished (1999)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: LDCM831 row: 1 column: 01
High quality sequence stop: 592.

FEATURES

Source

Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6598537"
/tissue_type="teratocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NH_MGC_109"
/note="Organ: ovary; Vector: pOTB7; Site 1: EcoRI; Site 2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGAGCAG(G). Library constructed by Ling Hong in the laboratory of Gerald W. Rubin (University of California, Berkeley) using Zap-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NH_MGC library."

ORIGIN

Query Match 3.5%; Score 186.6; DB 13; Length 710;
Best Local Similarity 81.3%; Pred. No. 3.9e-27;

Matches 231; Conservative 0; Mismatches 45; Indels 8; Gaps 1;

1321 ACCGTGCTCACTGCAACCTGCTGCTCCAGGTTCAAGCAATTCCTGCTCAGCCTCC 1380
646 ATCTCAGCTCACTGCAACCTGCTGCTCCAGGTTCAAGCAATTCCTGCTCAGCCTCC 587
1381 CGGTGCTGAGCTACAGGCG-----CAGCCCGGCTAATTTTGTATTTAGTA 1432
586 TGAGTAGCTGGAGTTACAGGCGCTGACACACGCGCGCTAATTTTGTATTTAGTA 527
1433 GAGATGGGTTTACCACTATTAGCCCGGCTGCTTGAATCTGAGCTCAGGTATCCA 1492
526 GAGATGGGTTTACCACTATTAGCCCGGCTGCTTGAATCTGAGCTCAGGTATCTG 467
1493 CCCACTCAGCTCCTTAAGTGTGGATTTACAGGATGAGTCAACGCGCGCCGCAAG 1552
466 CCCGCTCGGCTCCCAAGGTGGGATTTACAGGATGAGTCAACGCGCGCCGCAAG 407
1553 GTCACTGTTAATTAAGGATTAAGTGTGTTTCTAACCCTA 1596
406 TTCAGGTGCTTTTAAAGTAACTAATTTTATTTTACTTAA 363

RESULT 2 515 bp mRNA linear EST 31-DEC-2002
CA946732
LOCUS is09h12.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6364654 3',
DEFINITION mRNA sequence.
ACCESSION CA946732
VERSION CA946732.1 GI:27439609
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 515)
Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hiller, L., Marra, M., Page, D., Wylie, T., Martin, J., Blaisstein, A.,
Schmitt, A., Treising, B., Riltar, E., Bonio, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaratshvili, R.,
Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)

TITLE Unpublished (2000)
JOURNAL Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
COMMENT Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center for information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 451.
Location/Qualifiers
1. 515
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6364654"
/tissue_type="purified pancreatic islet"
/lab_host="DH10B"
/clone_id="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site 1:
NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permut Lab), Washington University
School of Medicine, Box 8157, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

FEATURES

Source

Query Match 3.5%; Score 182.4; DB 14; Length 515;
Best Local Similarity 86.4%; Pred. No. 2.9e-26;

Matches 216; Conservative 0; Mismatches 26; Indels 8; Gaps 1;

1321 ACCGTGCTCACTGCAACCTGCTGCTCCAGGTTCAAGCAATTCCTGCTCAGCCTCC 1380
46 ATCTCAGCTCACTGCAACCTGCTGCTCCAGGTTCAAGCAATTCCTGCTCAGCCTCC 105
1381 CGGTGCTGAGCTACAGGCG-----CAGCCCGGCTAATTTTGTATTTAGTA 1432
106 CAAGTAGCTGGAGTTACAGGCGACACACACGCGCGCTAATTTTGTATTTAGTA 165
1433 GAGATGGGTTTACCACTATTAGCCCGGCTGCTTGAATCTGAGCTCAGGTATCCA 1492
166 GAGATGGGTTTACCACTATTAGCCCGGCTGCTTGAATCTGAGCTCAGGTATCCA 225
1493 CCCACTCAGCTCCTTAAGTGTGGATTTACAGGATGAGTCAACGCGCGCCGCAAG 1552
226 CCCACTCAGCTCCTTAAGTGTGGATTTACAGGATGAGTCAACGCGCGCCGCAAG 285
1553 GTCACTGTTT 1562
286 TTTGTATTT 295

RESULT 3 660 bp DNA linear GSS 30-JUL-1998
AA057239
LOCUS CIT-HSP-2340D14.TR CIT-HSP Homo sapiens genomic clone 2340D14,
DEFINITION genomic survey sequence.
ACCESSION AA057239
VERSION AA057239.1 GI:3353765
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 660)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Baas, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Simon, M., and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)

TITLE Unpublished (1998)
JOURNAL Other GSSs: CIT-HSP-2340D14.TF
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC

end search page:

http://www.tigr.org/cdb/hungen/bac_end_search/bac_end_search.html.

Seq primer: M13 Reverse

Class: BAC ends.

FEATURES

source

Location/Qualifiers
1..660
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2340D14"
/sex="Male"
/cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBelOAC11, site_1: HindIII, site_2: HindIII"

ORIGIN

Query Match

Best Local Similarity 86.0%; Score 180.8; DB 28; Length 660;

Matches 215; Conservative 0; Mismatches 27; Indels 8; Gaps 1;

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QY 1321 ACCTGAGCTCAGTCAAGCACTCTGCTCCGAGTTCAAGCAATTCCTGCTCAGCCTCC 1380
DB 293 ATCTCACTCAGTCAAGCACTCTGCTCCGAGTTCAAGCAATTCCTGCTCAGCCTCC 352
QY 1381 CGCGTACTGAGTCAAGCACTCTGCTCCGAGTTCAAGCAATTCCTGCTCAGCCTCC 1432
DB 353 CAGTACTGAGTCAAGCACTCTGCTCCGAGTTCAAGCAATTCCTGCTCAGCCTCC 412
QY 1433 GAGTACTGAGTCAAGCACTCTGCTCCGAGTTCAAGCAATTCCTGCTCAGCCTCC 1492
DB 413 GAGTACTGAGTCAAGCACTCTGCTCCGAGTTCAAGCAATTCCTGCTCAGCCTCC 472
QY 1493 CCCACCTCAGCCTCTTAAGTGTGGATTACAGGATGATGATCAGCCGCGGCGCAAG 1552
DB 473 CCCACCTCAGCCTCTTAAGTGTGGATTACAGGATGATGATCAGCCGCGGCGCAAG 532
QY 1553 GTCAGTCTTT 1562
DB 533 TTTTGTATT 542

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RESULT 4

LOCUS AO379787 539 bp DNA linear GSS 20-MAY-1999

DEFINITION RPI11-152C3.TJ RPI1-11 Homo sapiens genomic clone RPI1-11-152C3,

genomic survey sequence.

ACCESSION AO379787

VERSION AO379787.1

KEYWORDS GI:4350810

SOURCE GSS.

ORGANISM Homo sapiens (human)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Map Building
Unpublished (1997)
Contact: Shaying Zhao, William Niernan, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hde@tigr.org

FEATURES

source

Location/Qualifiers
1..539
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/db_xref="taxon:9606"
/clone="RPI1-11-152C3"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPI1-11"
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RPI11 Human Male BAC Library"

ORIGIN

Query Match

Best Local Similarity 76.8%; Score 179.8; DB 28; Length 539;

Matches 235; Conservative 0; Mismatches 63; Indels 8; Gaps 1;

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QY 1280 AGGATGAGGCTCTGTCTTTTACACCTGATGCTCTACACCTGAGCTCAGCAACC 1339
DB 327 AGAGTCTGCTCTGTCTTTTACACCTGATGCTCTACACCTGAGCTCAGCAACC 268
QY 1340 TCTGCTCCCGAGTTCAAGCAATTCCTGCTCAGCCTCCGAGTTAGTGGAGTAAG 1399
DB 267 TCTGCTCCCGAGTTCAAGCAATTCCTGCTCAGCCTCCGAGTTAGTGGAGTAAG 208
QY 1400 GC-----GCAAGCCCGGCTAATTTTGTATTTTATTTATTTATTTATTTATTT 1451
DB 207 GCATGTGCAACCAATACCCGCTAATTTTGTATTTTATTTATTTATTTATTTATTT 148
QY 1452 TTAGCCCGGCTGCTGCTTTGAACCTGACCTCAGGTATCCACCACTCAGCCTCTAA 1511
DB 147 TTGACCAAGCTGCTGCTTTGAACCTGACCTCAGGTATCCACCACTCAGCCTCTAA 88
QY 1512 GTGCTGGATTACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1571
DB 87 GTGCTGGATTACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 28
QY 1572 TTAATT 1577
DB 27 TGAATT 22

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RESULT 5

LOCUS BU957861/c 340 bp mRNA linear EST 21-OCT-2002

DEFINITION AGENCOURT_1062879 NIH_MGC_141 Homo sapiens cDNA clone

IMAGE:6731972 5', mRNA sequence.

ACCESSION BU957861

VERSION BU957861.1

KEYWORDS GI:24187433

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: gsabbs-remail.nih.gov
Tissue Procurement: NCI
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>

High quality sequence stop: 619.

Location/Qualifiers

1..887

Query Match	3.4%;	Score 178.6;	DB 12;	Length 887;
Best Local Similarity	77.6%;	Pred. No. 1.6e-25;		
Matches 232; Conservative	0;	Mismatches 59;	Indels 8;	Gaps 1;

QY	1281	3GGGTAGAGGGTGTGTGTTCACCTACCTATGCTCTACACCTGAGCGCATCGAACCT	1340
Db	427	GAGTCTGCTGTGTGGCCAGGCGTAGGCGCACTGSCATGATCTCTGCTCACTGCACAT	368
QY	1341	CTGCTCCGAGTTCAGCAATCTCTGTCTGAGCTCCGCGTAGCTGGGACATCAGG	1400
Db	367	CGGCTCCGAGGTTCAAGCAATCTCTGCTGAGCTCCGAGTAGCTGGGATTACGG	308
QY	1401	C-----GAGCGCGGGCTATTTTGTATGTATGATAGAGATGGGTTTACACAT	1452
Db	307	CTGTGCGACCAACCGCCGGCTAATTTTGTATTTTGTAGAGAGACGGGGTTTCTCACT	248
QY	1453	TAGCCCGGCTGTGTTGAACTCTTGAACCTGAGTGATCCACCACTTACGCTCTTAAG	1512
Db	247	TGGCCAGGCTGTGTTGAACTCTTGAACCTGAGTGATCCACCACTTCCGCTCCCAAG	188
QY	1513	TGTGGAGTTACAGGCGATGATCACCGCGCGCGCAGAGGTCAAGTGTTTAATAAGAA	1571
Db	187	TGTGGAGTTACAGGAGTAGACCCCGCACCCGCGCTTAATACACTTTTAACGTGAA	129

LOCUS	AM978041	537 bp	mRNA	linear	EST 02-JUN-2000
DEFINITION	ESR390150	MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.			
ACCESSION	AM978041				
VERSION	AM978041.1	GI:8169303			

SOURCE	Homio sapiens (human)
ORGANISM	Homio sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt,J.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.
TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
JOURNAL	Unpublished (2000)
COMMENT	Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208

Email: johnq@ligr.org
 Plate: 387
 Seq primer: Forward.
 Location/Qualifiers
 1..537
 /organism="Homo sapiens"
 /mol_type="rRNA"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE resequences, YAGO"
 /note="Vector: pBluescriptSKm"

ORIGIN

Query Match 3.4%; Score 178.4; DB 10; Length 537;
 Best Local Similarity 77.2%; Pred. No. 1.8e-25;
 Matches 233; Conservative 0; Mismatches 61; Indels 8; Gaps 1;

OY 1281 GGGTGAAGGCTCTGTCTTACCTACCTGATGCTCTACCTGAGCTCACTGCAACCT 1340
 Db 6 GAGTCTGTCTGTGTCCAGAGCTGAGTGCATGTCATGATCTCGGCTCACTGCAAACT 65
 OY 1341 CTGCTCTCCAGTTCAGCAATTCCTCTCTCAAGCTCCCGTACGAGGAGTACAG 1400
 Db 66 CCACCTCCCAAGTTCAGCAATTCCTCTCTCAAGCTCCCGTACGAGGAGTACAG 125
 OY 1401 CG-----CAGCCCGGCTAATTTTGTATTGTATTAGATGAGATGGGGTTTCAACCAT 1452
 Db 126 TGCCCAACACCAACACCACTAATTTTGTATTAGATGAGATGGGGTTTCAACCAT 1485
 OY 1453 TAGCCCGGCTGTCTTGAACCTCTGACCTCAAGTATCAACCACTCAAGCTCTTAAG 1512
 Db 186 TGCCAGACTGTCTCCAGCTCTGACCTCAAGTATCAACCACTCAAGCTCTTAAG 245
 OY 1513 TGCTGGGATTACAGGATGATGATCAGCGCGCGGCAAGGATGATGATTAAGGAT 1572
 Db 246 TGCTGGGATTACAGGATGATGATCAGCGCGCGGCTTGGACAGGATCTTTAAGGAG 305
 OY 1573 AA 1574
 Db 306 AA 307

RESULT 12
 BM803650 LOCUS 990 bp rRNA linear EST 05-MAR-2002
 AGENCOURT 6439541 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5520297

DEFINITION 5' mRNA sequence.
 ACCESSION BM803650.1 GI:19120473
 VERSION
 KEYWORDS
 ORGANISM

EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 990)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM12184 row: b column: 10
 High quality sequence stop: 632.
 Location/Qualifiers

FEATURES

1..990
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"

/clone="IMAGE:5520297"
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 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 2.1 kb."

ORIGIN

Query Match 3.4%; Score 177.8; DB 12; Length 990;
 Best Local Similarity 82.9%; Pred. No. 2.3e-25;
 Matches 218; Conservative 0; Mismatches 37; Indels 8; Gaps 1;

OY 1327 GCTCAGTCACTCTGCTCCAGGTTCAACCAATTCCTGTCTCAAGCTCCCGGTA 1386
 Db 97 GCTTACTGCACTCTCACTCCAGGATCAATGATTCCTGCTCAAGCTCCCGGTA 156
 OY 1387 GCTGGAGCTACAGCG-----CAGCCCGGCTAATTTTGTATTGTAGTAGAGTG 1438
 Db 157 GCTGGAGTACAGCGCCCGGCAACATGCAAGCTAATTTTGTATTGTAGTAGAGTG 216
 OY 1439 GGGTTTACCATATTAGCCCGGCTGCTTGAATCTGACCTCAAGTATCAACCAAC 1498
 Db 217 AGGTTTACCATATTAGCCCGGCTGCTTGAATCTGACCTCAAGTATCAACCAAC 276
 OY 1499 TCAGCTCTTAAGTCTGGGATTTACAGGATGATGATCAGCGCGCGGCAAGGCTAGT 1558
 Db 277 TCAGCTCTTAAGTCTGGGATTTACAGGATGATGATCAGCGCGCGGCAAGGCTAGT 336
 OY 1559 GTTTAATAGGATTAATTAAT 1581
 Db 337 AATTTTAAGGATTAATTAAT 359

RESULT 13

AO112451 LOCUS 516 bp DNA linear GSS 29-AUG-1998
 CIT-HSP-2372C9.TF CIT-HSP Homo sapiens genomic clone 2372C9,
 genomic survey sequence.

ACCESSION AO112451
 VERSION AO112451.1 GI:3484611
 KEYWORDS
 ORGANISM

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 516)
 Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
 Berry,K., Granger,D., Suh,E., White,C., Shizuya,H., Simon,M. and
 Venter,J.C.
 Use of a random human BAC End Sequence Database for Sequence-Ready
 Map Building
 Unpublished (1998)
 Other GSSs: CIT-HSP-2372C9.TF
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: madams@ligr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.ligr.org/tbld/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.
 Location/Qualifiers

FEATURES

1..516
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ORIGIN

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Best Local Similarity 85.2%; Pred. No. 2.7e-25;
Matches 213; Conservative 0; Mismatches 29; Indels 8; Gaps 1;

QY 1321 ACCTGAGCTACATGGAACCTGCTCCGAGGTTGAGAAATTTCTGTCACAGCTCC 1380
DB 255 ATCTGAGCTACATGGAACCTGCTCCGAGGTTGAGAAATTTCTGTCACAGCTCC 314
QY 1381 CGGCTAGCTGGAGCTACAGGCG-----CAGCCCGGCTAATTTTGTATTTAGTA 1432
DB 315 CAGTACCTGAGTATACAGGCGCAGCAGAGCCCGGCTAATTTTGTATTTAGTA 374
QY 1433 GAGATGGGCTTACCATATTAAGCCGCTGCTGTTGAATCTGTAAGCTCAGTGATCA 1492
DB 375 GAGATGGGCTTACCATATTAAGCCGCTGCTGTTGAATCTGTAAGCTCAGTGATCA 434
QY 1493 CCCACCTGAGCTCTCTAAAGTGTGAGATTACAGCATAGTCAAGCGCCGCGCAAG 1552
DB 435 CCCACCTGAGCTCTCTAAAGTGTGAGATTACAGCATAGTCAAGCGCCGCGCAAG 494
QY 1553 GTGAGTCTTT 1562
DB 495 TTTTGCAATT 504

RESULT 14
AO265389 577 bp DNA linear GSS 27-OCT-1998
LOCUS AO265389/c
DEFINITION CITBI-EI-2509010.TF CITBI-EI Homo sapiens genomic clone 2509010,
genomic survey sequence.
ACCESSION AO265389
VERSION AO265389.1 GI:3793589
KEYWORDS GSS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 577)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Liner,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
JOURNAL Unpublished (1998)
COMMENT Other GSSs: CITBI-EI-2509010.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Classes: BAC ends.
Location/Qualifiers
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FEATURES
source

Caltech Human BAC Library D"

ORIGIN

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Best Local Similarity 75.1%; Pred. No. 2.9e-25;
Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;

QY 1321 ACCTGAGCTACATGGAACCTGCTCCGAGGTTGAGAAATTTCTGTCACAGCTCC 1380
DB 368 ATCTGAGCTACATGGAACCTGCTCCGAGGTTGAGAAATTTCTGTCACAGCTCC 309
QY 1381 CGGCTAGCTGGAGCTACAGGCG-----GAGCCCGGCTAATTTTGTATTTAGTA 1432
DB 308 CAGTACCTGAGTATACAGGCGCAGCAGAGCCCGGCTAATTTTGTATTTAGTA 249
QY 1433 GAGATGGGCTTACCATATTAAGCCGCTGCTGTTGAATCTGTAAGCTCAGTGATCA 1492
DB 248 GAGATGGGCTTACCATATTAAGCCGCTGCTGTTGAATCTGTAAGCTCAGTGATCA 189
QY 1493 CCCACCTGAGCTCTCTAAAGTGTGAGATTACAGCATAGTCAAGCGCCGCGCAAG 1552
DB 188 CCCACCTGAGCTCTCTAAAGTGTGAGATTACAGCATAGTCAAGCGCCGCGCAAG 129
QY 1553 GTGAGTCTTTATAGAAATCTGTAATGTTTACTAAACCAAGGAAACAGACAA 1612
DB 128 GATACATTTTGTAAATTAAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 69
QY 1613 AGCTGTGATTAATTTGAG 1629
DB 68 AGTAACTAGTATGAG 52

RESULT 15
A1583291 548 bp mRNA linear EST 14-DEC-1999
LOCUS A1583291/c
DEFINITION t156902.x1 NCI CGAP HSC4 Homo sapiens CDNA clone IMAGE:2244818.3,
similar to TR:013538 O13538 ORF2; FUNCTION UNKNOWN; contains Alu
repetitive element; mRNA sequence.
ACCESSION A1583291
VERSION A1583291.1 GI:4569188
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 548)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cgs@ps-remail.nih.gov
Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/INL at:
www.bio.lnlnl.gov/bdip/image/image.html
Insert Length: 664 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 464
POLYA=No.
Location/Qualifiers
1..548
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/clone_lib="NCI-CGAP_HSC4"

FEATURES
source

/note="Organ: bone marrow; Vector: pAMP1; mRNA made from lymphoid tissue, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified. cDNA Library Preparation: David B. Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

ORIGIN

Query Match 3.4%; Score 177.2; DB 9; Length 548;
 Best Local Similarity 78.8%; Pred. No. 3.2e-25;
 Matches 227; Conservative 0; Mismatches 53; Indels 8; Gaps 1;

QY	1277	GTGAGGAGTGAAGGCTGTGTGCTTACACCTACCTGATGCTCTACACCTGAGCTCACTGCA	1336
DB	546	GAGGAGATCTTGATCTGTCTCAGGCTGAGTGCAGTGCATGATCTTGCTCACTGCA	487
QY	1337	ACCTCTGCTCTCCAGGTTCAAGCAATTCTCTGTCTCAGCTCTCCGCTGAGCTGAGCTA	1396
DB	486	ACCTCCGCTCTCAGGTTCAAGCAATTCTCTGCTCAGCTCTCCGCTGAGCTGAGCTA	427
QY	1397	CAGGCG-----CAGCGCCGGCTAATTTTGTATTGTAGTAGAGATGAGGTTTCAAC	1448
DB	426	CAGGCGCCGCCACGAGCTGCTAATTTTGTATTGTAGTAGAGATGAGGTTTCAAC	367
QY	1449	ATATTAGCCCGCTGTGTCTTGAACCTCTGACCTCAGGTGATCCACCCACCTCAGCTCTCT	1508
DB	366	ATGTTGACCAAGGCTGTGTGAACCTCTGACCTCAGGTGATCCACCCACCTTGTCTCTCC	307
QY	1509	AAAGTCTGGGATTACAGGCATGAGTACCGGCGCCGCCAAGGCTCA	1556
DB	306	AAAGTCTGGGATTACAGGCATGAGTACCGGCGCCGCCAAGGATTCA	259

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 Job time : 12235 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 19, 2004, 12:16:22 ; Search time 2222 Seconds
(without alignments)
11973.488 Million cell updates/sec

Title: US-09-227-881-34

Sequence: 1 atccttgcagttcactc.....tcgggcattgagccagcaag 5271

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3327077 seqs, 2523723180 residues

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

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4. /cgm2_6/p10data/2/pubnpa/US06_PUBCOMB.seq.*
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7. /cgm2_6/p10data/2/pubnpa/US08_NEW_PUB.seq.*
8. /cgm2_6/p10data/2/pubnpa/US08_PUBCOMB.seq.*
9. /cgm2_6/p10data/2/pubnpa/US09_PUBCOMB.seq.*
10. /cgm2_6/p10data/2/pubnpa/US09B_PUBCOMB.seq.*
11. /cgm2_6/p10data/2/pubnpa/US09C_PUBCOMB.seq.*
12. /cgm2_6/p10data/2/pubnpa/US09C_NEW_PUB.seq.*
13. /cgm2_6/p10data/2/pubnpa/US09C_NEW_PUB.seq.*
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15. /cgm2_6/p10data/2/pubnpa/US10B_PUBCOMB.seq.*
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18. /cgm2_6/p10data/2/pubnpa/US60_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5271	100.0	5271	15	US-10-244-633-34	Sequence 34, Appl
2	5271	100.0	6169	15	US-10-244-633-3	Sequence 3, Appl
3	5246.4	99.5	5300	10	US-09-985-637A-1	Sequence 1, Appl
4	5246.4	99.5	5300	15	US-10-244-633-1	Sequence 1, Appl
5	5246.4	99.5	5300	17	US-10-741-339-1	Sequence 1, Appl
6	5232.4	99.3	37252	13	US-10-087-132-228	Sequence 128, Ap
7	5224.4	99.1	5304	15	US-10-244-633-2	Sequence 2, Appl
8	1804.4	34.2	2800	10	US-09-952-464A-1	Sequence 1, Appl
9	1804.4	34.2	2800	15	US-10-011-870-10	Sequence 10, Appl
10	394.4	7.5	1086	13	US-10-244-425-1586	Sequence 1586, Ap
11	227	4.3	227	15	US-10-244-633-38	Sequence 38, Appl
12	227	4.3	283	15	US-10-244-633-37	Sequence 37, Appl
13	222.6	4.2	30057	14	US-10-087-132-4225	Sequence 1225, Ap
14	185.4	3.5	86361	17	US-10-741-601-5702	Sequence 5702, Ap

C 15	184.4	3.5	1744	16	US-10-104-047-1845	Sequence 1845, App
C 16	184.2	3.5	70779	13	US-10-087-192-1012	Sequence 1012, App
C 17	183.2	3.5	41936	9	US-09-967-7684-116	Sequence 116, App
C 18	183.2	3.5	104245	13	US-10-665-847-4	Sequence 4, Appl
C 19	183.2	3.5	104345	13	US-10-160-807-4	Sequence 4, Appl
C 20	181.2	3.5	170345	17	US-10-317-597-322	Sequence 322, Appl
C 21	181.2	3.4	196063	17	US-10-322-281-612	Sequence 612, App
C 22	180.6	3.4	39725	15	US-10-017-61-1611	Sequence 1611, App
C 23	180.6	3.4	39729	16	US-10-292-798-1285	Sequence 1285, App
C 24	180.6	3.4	66333	13	US-10-182-936A-11	Sequence 11, Appl
C 25	180.6	3.4	66333	16	US-10-374-979-11	Sequence 11, Appl
C 26	180.6	3.4	66333	17	US-10-731-739-11	Sequence 11, Appl
C 27	180.6	3.4	72049	13	US-10-382-936A-9	Sequence 9, Appl
C 28	180.6	3.4	72049	16	US-10-374-979-9	Sequence 9, Appl
C 29	180.6	3.4	72049	17	US-10-731-739-9	Sequence 9, Appl
C 30	180.6	3.4	156643	13	US-10-087-192-1408	Sequence 1408, App
C 31	179.8	3.4	100301	17	US-10-430-826-83	Sequence 83, Appl
C 32	179.6	3.4	81968	17	US-10-332-696-142	Sequence 142, Appl
C 33	179.6	3.4	653122	13	US-10-087-192-126	Sequence 226, App
C 34	179.4	3.4	10348	15	US-10-017-161-2065	Sequence 2069, App
C 35	179.4	3.4	10348	16	US-10-292-798-1715	Sequence 1715, App
C 36	179.4	3.4	304805	13	US-10-721-416-1	Sequence 1, Appl
C 37	179.2	3.4	6708	10	US-09-764-891-6566	Sequence 6566, App
C 38	179.2	3.4	6708	15	US-10-205-428-761	Sequence 761, App
C 39	179.2	3.4	299598	17	US-10-332-696-16	Sequence 16, Appl
C 40	179	3.4	300000	15	US-10-262-552-33	Sequence 33, Appl
C 41	178.8	3.4	81968	17	US-10-733-210-33	Sequence 33, Appl
C 42	178.6	3.4	212231	13	US-10-372-696-142	Sequence 142, App
C 43	178.6	3.4	518360	17	US-10-087-192-1126	Sequence 1126, App
C 44	178.4	3.4	518360	17	US-10-367-094-125	Sequence 125, App
C 45	178.4	3.4	127917	17	US-10-775-169-82	Sequence 82, Appl

ALIGNMENTS

RESULT 1

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Sequence 34 Application US/10244433
Publication No. US20030068640A1
GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
APPLICANT: Chen, Pu
APPLICANT: Chen, Hua
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
TITLE OF INVENTION: Disorders
FILE REFERENCE: 07425.0057.US01
CURRENT APPLICATION NUMBER: US/10/244,633
CURRENT FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: US/09/306,828
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/227,861
PRIOR FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft word 97
SEQ ID NO 34
LENGTH: 5271
TYPE: DNA
ORGANISM: Homo sapiens
US-10-244-633-34

Query Match          100.0%   Score 5271;   DB 15;   Length 5271;
Best Local Similarity 100.0%   Pred. No. 0;
Matches 5271;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0

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Db 61 TCTATAAAGCTGTAAGCTCCATTCGATGTAATGCTTTGGCAGATGATTAAGATCA 120
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Db 121 GGAAGAGAGATATCCACGTTAGCCAAAGTGTCCAGGCTGTGTCTCTTAATTTAGTGA 180
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5161 CCGTGTGACAG 5220
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PRIOR FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Word 97
SEQ ID NO: 3
LENGTH: 6169
TYPE: DNA
ORGANISM: Homo sapiens
US-10-244-633-3
Query Match 100.0%; Score 5271; DB 15; Length 6169;
Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;
Matches 5271; Conservative 0; Mismatches 0; Gaps 0;
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1 ATCTTTGCTCACTTACCTCAAGGCTATTAAGAAATGAAATGAAATGAAATGAAATG 60
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 US-10-244-633-1
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 ; Publication No. US2003068640A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nguyen, Thai D.
 ; APPLICANT: Polansky, Jon R.
 ; APPLICANT: Chen, Pu
 ; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
 ; TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
 ; TITLE OF INVENTION: Disorders
 ; FILE REFERENCE: 07425.0057.US01
 ; CURRENT APPLICATION NUMBER: US/10/244,633
 ; CURRENT FILING DATE: 2002-09-17
 ; PRIOR APPLICATION NUMBER: US/09/306,828
 ; PRIOR FILING DATE: 1999-05-07
 ; PRIOR APPLICATION NUMBER: US 09/227,881
 ; PRIOR FILING DATE: 1999-01-11
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: Microsoft Word 97
 ; SEQ ID NO 1
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 DB 241 CATTAACAGAGCTAAGAAACAGAAATGAGATGGCACTTGGCCCAAGAAATGCGCAG 300
 QY 301 GAGAGCAATATGATGAAATATAAATCTTCCCTTGTGTTTAAATTTACAGAAAAATG 360
 DB 301 GAGAGCAATATGATGAAATATAAATCTTCCCTTGTGTTTAAATTTACAGAAAAATG 360
 QY 361 ATGAGACCAAAATCAATGATTAAGAAACAGCTCAGAAAAAAGATGTTTCAAAATGG 420
 DB 361 ATGAGACCAAAATCAATGATTAAGAAACAGCTCAGAAAAAAGATGTTTCAAAATGG 420
 QY 421 TAATTAAGATTTTGTCTTGGGAGAGCTTCATGTAGCTGTGAGTGAAGTGGGA 480

Db 421 TAAATTAAGTATTTGCTTCCTTGGGAAAGACCTCCATGTGAGCTTGATGGGAAAAATGGGA 480
QY 481 AAAAGTCAAAAAGCATATGTGATCAGATCCAAAGTGAATTTATTTTAAAAAACAAGAT 540
Db 481 AAAAGTCAAAAAGCATATGTGATCAGATCCAAAGTGAATTTATTTTAAAAAACAAGAT 540
QY 541 GGGATCACTCTGGGAGGAGGAGTTGAGAGAGTCAATGTTAGCAAAAGSACATTAACATPAC 600
Db 541 GGGATCACTCTGGGAGGAGGAGTTGAGAGAGTCAATGTTAGCAAAAGSACATTAACATPAC 600
QY 601 AGCAAAATCAAAATTCGCGAAAATGCAAGAGAAAATGGGGAATGGGAAAGCTTTTCAATAC 660
Db 601 AGCAAAATCAAAATTCGCGAAAATGCAAGAGAAAATGGGGAATGGGAAAGCTTTTCAATAC 660
QY 661 AGTGAATTAAGGAGTGAACATGTTGCGCAACACTCCGCTATPCCAGGAGCAACAAAA 720
Db 661 AGTGAATTAAGGAGTGAACATGTTGCGCAACACTCCGCTATPCCAGGAGCAACAAAA 720
QY 721 ATTGAATGGGCTAAAGCTGACCTTTCAAGGAAAATGTAATAAACTGAGAGCAAAACAAA 780
Db 721 ATTGAATGGGCTAAAGCTGACCTTTCAAGGAAAATGTAATAAACTGAGAGCAAAACAAA 780
QY 781 GACATGGTTAAAGGAGCAACGAACTTTGTAGCTTTCAAGAGCAAGTGCCTTCAGCA 840
Db 781 GACATGGTTAAAGGAGCAACGAACTTTGTAGCTTTCAAGAGCAAGTGCCTTCAGCA 840
QY 841 GGGAGCCTGAGCATTTGCTTTAGGAGGCGAGTTTCTTAAGGATCTTAAGAAATC 900
Db 841 GGGAGCCTGAGCATTTGCTTTAGGAGGCGAGTTTCTTAAGGATCTTAAGAAATC 900
QY 901 TTGAAAGATCATGAATTTTAACTTTAAGTCAAGGATTAAGTCAAGGATTAAGTCAAG 960
Db 901 TTGAAAGATCATGAATTTTAACTTTAAGTCAAGGATTAAGTCAAGGATTAAGTCAAG 960
QY 961 TTGAGCAATGGGTCCTCAATTTTAAAGTCAAGGATTAAGTCAAGGATTAAGTCAAG 1020
Db 961 TTGAGCAATGGGTCCTCAATTTTAAAGTCAAGGATTAAGTCAAGGATTAAGTCAAG 1020
QY 1021 GGAATAGGTCAGAAATCATTTAGAAATCATGTGTCCCACTTAACTTTTCAAGATGATC 1080
Db 1021 GGAATAGGTCAGAAATCATTTAGAAATCATGTGTCCCACTTAACTTTTCAAGATGATC 1080
QY 1081 TGTGATAGCCCTCAACACAGAGGCGGATGTGTGATGATCAACACAGAGTCAACACCA 1140
Db 1081 TGTGATAGCCCTCAACACAGAGGCGGATGTGTGATGATCAACACAGAGTCAACACCA 1140
QY 1141 GTGCTCTCAACATTTTAACTTTAAGTCAAGGATTAAGTCAAGGATTAAGTCAAG 1200
Db 1141 GTGCTCTCAACATTTTAACTTTAAGTCAAGGATTAAGTCAAGGATTAAGTCAAG 1200
QY 1201 TGTGAGAGCCCATCCGCTCAACAGAGGATGTGTGATGATCAACACAGAGTCAACACCA 1260
Db 1201 TGTGAGAGCCCATCCGCTCAACAGAGGATGTGTGATGATCAACACAGAGTCAACACCA 1260
QY 1261 TACAGAGAGAGTCTGCTGAGGAGTGTGTGATGATCAACACAGAGTCAACACCA 1320
Db 1261 TACAGAGAGAGTCTGCTGAGGAGTGTGTGATGATCAACACAGAGTCAACACCA 1320
QY 1321 ACCTGAGCTCACTGCAACCTTGTGCTCCAGAGTCAAGCAATTCCTGCTCAAGCTCC 1380
Db 1321 ACCTGAGCTCACTGCAACCTTGTGCTCCAGAGTCAAGCAATTCCTGCTCAAGCTCC 1380
QY 1381 CGGATAGCTGAGGAGTCAAGAGGAGGAGGAGTGTGTGATGATCAACACAGAGTCAACACCA 1440
Db 1381 CGGATAGCTGAGGAGTCAAGAGGAGGAGGAGTGTGTGATGATCAACACAGAGTCAACACCA 1440
QY 1441 GTTTCACCAATTAAGCTGCTGCTGCTTGAACCTTCAAGTCAAGTCAAGTCAAG 1500
Db 1441 GTTTCACCAATTAAGCTGCTGCTGCTTGAACCTTCAAGTCAAGTCAAGTCAAG 1500
QY 1501 AGCTCTCTAAAGTGTGAGGATTAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAG 1560
Db 1501 AGCTCTCTAAAGTGTGAGGATTAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAG 1560

QY 1561 TTAAATAGGAATTAAGTGAATGTTTACTAAACCAAGAGGAAAAGAGAAAGCTGTGA 1620
Db 1561 TTAAATAGGAATTAAGTGAATGTTTACTAAACCAAGAGGAAAAGAGAAAGCTGTGA 1620
QY 1621 TAATTTACGAGATTTCTTGGAGTGGGGAATGGTGCATAGCTGCTGCTTATGCCAGAC 1680
Db 1621 TAATTTACGAGATTTCTTGGAGTGGGGAATGGTGCATAGCTGCTGCTTATGCCAGAC 1680
QY 1681 CACTGCTCTCATCACTTTCTTCTTCTCATCTCTCAATTTTTCAGGCTTAAGTTTATTTAT 1740
Db 1681 CACTGCTCTCATCACTTTCTTCTTCTCATCTCTCAATTTTTCAGGCTTAAGTTTATTTAT 1740
QY 1741 CACATGCTTTTGTGTAAGCTTCAATCGTTACTGAAATTAAGATATCATTAACCTAG 1800
Db 1741 CACATGCTTTTGTGTAAGCTTCAATCGTTACTGAAATTAAGATATCATTAACCTAG 1800
QY 1801 TTTCATTTGGGGCCATCTGTGTGTGTATPAGGAGAGAGGAGCAATCCAGAGACTCTCT 1860
Db 1801 TTTCATTTGGGGCCATCTGTGTGTGTATPAGGAGAGAGGAGCAATCCAGAGACTCTCT 1860
QY 1861 TGAAGCCCCCGGAGAGGTTTCTCTCAGCTGAGGAGGCTTCAGAGCAACCCGAGGCTC 1920
Db 1861 TGAAGCCCCCGGAGAGGTTTCTCTCAGCTGAGGAGGCTTCAGAGCAACCCGAGGCTC 1920
QY 1921 TGGATGCTCTGAGCAACCTGCAAGCCGCTGCACTGATGTTTGTATGACTCTCTAG 1980
Db 1921 TGGATGCTCTGAGCAACCTGCAAGCCGCTGCACTGATGTTTGTATGACTCTCTAG 1980
QY 1981 GACCTGTTCTTCTTATTTCTGTGTGATCTGTTCAATCAACAGGATTAATGAGCAAT 2040
Db 1981 GACCTGTTCTTCTTATTTCTGTGTGATCTGTTCAATCAACAGGATTAATGAGCAAT 2040
QY 2041 TATTAAGTACTTATATCTGAGACACACAGAGCAAAATGATGAGCAAAAGCACTCTG 2100
Db 2041 TATTAAGTACTTATATCTGAGACACACAGAGCAAAATGATGAGCAAAAGCACTCTG 2100
QY 2101 CCTACCTTGTGAGAGTGAACATTTCTCATGAGAGAGCTGAGAGAGAAATTAATAGCA 2160
Db 2101 CCTACCTTGTGAGAGTGAACATTTCTCATGAGAGAGCTGAGAGAGAAATTAATAGCA 2160
QY 2161 GCAACTTAAACCCAGAGTCTGAGAGAGAGAGAAATTAACAACATCTTGAAGAAATGTCG 2220
Db 2161 GCAACTTAAACCCAGAGTCTGAGAGAGAGAGAGAAATTAACAACATCTTGAAGAAATGTCG 2220
QY 2221 AGCATCTCTTAAACAGGCTCTCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2280
Db 2221 AGCATCTCTTAAACAGGCTCTCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2280
QY 2281 GCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2340
Db 2281 GCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2340
QY 2341 GCTGCTCTTCCGAGTAAATGATCTGTGTGATCTGAGTGAAGTCTTGTGCTCAAGGCT 2400
Db 2341 GCTGCTCTTCCGAGTAAATGATCTGTGTGATCTGAGTGAAGTCTTGTGCTCAAGGCT 2400
QY 2401 CAG 2460
Db 2401 CAG 2460
QY 2461 CTCAG 2520
Db 2461 CTCAG 2520
QY 2521 TGGGAGAGCTGAGGAGTGAAGGAGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 2580
Db 2521 TGGGAGAGCTGAGGAGTGAAGGAGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 2580
QY 2581 GCTGAG 2640
Db 2581 GCTGAG 2640

QY 2641 CTTTATCTTCTGCTTGAGAGAGAAAGTCTATTTCATGAGAGGATCAGTTTC 2700
Db 2641 CTTTATCTTCTGCTTGAGAGAGAAAGTCTATTTCATGAGAGGATCAGTTTC 2700
QY 2701 ATAAAGTCAGCTGTTAAATTCAGAGGTCGATGGCTTTCTTCACAGAGGCTTTAT 2760
Db 2701 ATAAAGTCAGCTGTTAAATTCAGAGGTCGATGGCTTTCTTCACAGAGGCTTTAT 2760
QY 2761 TTAATGGGAATATAGAGAGGAGCTCATTTCTAGGAGCTTAATTCACGGAATAATGAC 2820
Db 2761 TTAATGGGAATATAGAGAGGAGCTCATTTCTAGGAGCTTAATTCACGGAATAATGAC 2820
QY 2821 TGGAGCTTTTCTTCAATGCTCTGAGCAACTACTAGGCTGTGGTGAATTTGCTTA 2880
Db 2821 TGGAGCTTTTCTTCAATGCTCTGAGCAACTACTAGGCTGTGGTGAATTTGCTTA 2880
QY 2881 TGCAGAGCGTCGAAAACCTTGAATCAGAGAGCTGGTTTCTTTCTGCTTTCGCAAT 2940
Db 2881 TGCAGAGCGTCGAAAACCTTGAATCAGAGAGCTGGTTTCTTTCTGCTTTCGCAAT 2940
QY 2941 GATTGGCTGTGCGAACCGGAGGCAAGTGTCTCTCTGCTGGGCAATGCTCTGCTGT 3000
Db 2941 GATTGGCTGTGCGAACCGGAGGCAAGTGTCTCTCTGCTGGGCAATGCTCTGCTGT 3000
QY 3001 ATAAAGACCTTGCAGCTCTGCTGCTGCTGCACTTCCCTGATTTCTGAGAGGG 3060
Db 3001 ATAAAGACCTTGCAGCTCTGCTGCTGCTGCACTTCCCTGATTTCTGAGAGGG 3060
QY 3061 GAGTCTTGAAGGGGAGAGAGAGGAGAGCTGAGAGAGCTGAGCCAGAGAGGAGGAGG 3120
Db 3061 GAGTCTTGAAGGGGAGAGAGAGGAGAGCTGAGAGAGCTGAGCCAGAGAGGAGGAGG 3120
QY 3121 GGAACAGAGGAGGAGAGAGAGAGGAGGAGTGTCTCATCACTGATCACTGACAGCTC 3180
Db 3121 GGAACAGAGGAGGAGAGAGAGAGGAGGAGTGTGTCTCATCACTGATCACTGACAGCTC 3180
QY 3181 CAGAGCCGAGAGCCCAATGCTTCAAGAAAGCTCAATGAACCCACAGCCACATTTTCT 3240
Db 3181 CAGAGCCGAGAGCCCAATGCTTCAAGAAAGCTCAATGAACCCACAGCCACATTTTCT 3240
QY 3241 TCCCTAAGCATAGACATGAGCATTTGCAATTAACAAAGGAATGAGAGACATGAGT 3300
Db 3241 TCCCTAAGCATAGACATGAGCATTTGCAATTAACAAAGGAATGAGAGACATGAGT 3300
QY 3301 GGTAGCTTTGCTGAGCTTCAAAAACCTGGCCAGAGCAAGTGGAATTCAGAGATTG 3360
Db 3301 GGTAGCTTTGCTGAGCTTCAAAAACCTGGCCAGAGCAAGTGGAATTCAGAGATTG 3360
QY 3361 TTAACCTTTCAACCTGACAGAGCCCAAGAGCTGAGAGAGAGCTGAGAGAGAGG 3420
Db 3361 TTAACCTTTCAACCTGACAGAGCCCAAGAGCTGAGAGAGAGCTGAGAGAGAGG 3420
QY 3421 AGTACCTGAGAGGAG 3480
Db 3421 AGTACCTGAGAGGAG 3480
QY 3481 ACAAGTTCATCAAG 3540
Db 3481 ACAAGTTCATCAAG 3540
QY 3541 GTTCTAG 3600
Db 3541 GTTCTAG 3600
QY 3601 CCTGATTTCTAATCTAATATTTTCTTACAGCTGATTAATTCAGCAAGTCAAG 3660
Db 3601 CCTGATTTCTAATCTAATATTTTCTTACAGCTGATTAATTCAGCAAGTCAAG 3660
QY 3661 GTAGTAACAG 3720
Db 3661 GTAGTAACAG 3720
QY 3721 GGAAGTACAG 3780

Db 3721 GGAAGTACAG 3780
QY 3781 TAAAGCCAAACAGATTCAGAGCTTGTGCTGACTATATGATTTGGTTTTGAAAAT 3840
Db 3781 TAAAGCCAAACAGATTCAGAGCTTGTGCTGACTATATGATTTGGTTTTGAAAAT 3840
QY 3841 CATTGAG 3900
Db 3841 CATTGAG 3900
QY 3901 TAAACAAACCCAGTTGTAATGCTCAAGTTCAGGCTTAATCTGAGAGAGAGAGAG 3959
Db 3901 TAAACAAACCCAGTTGTAATGCTCAAGTTCAGGCTTAATCTGAGAGAGAGAGAG 3960
QY 3960 AAGATAG 4019
Db 3961 AAGATAG 4019
QY 4020 CAGTTGGAAATATTTACTTCAAGAGATGACAGTGTGTTGATTAACAAATTAAG 4079
Db 4020 CAGTTGGAAATATTTACTTCAAGAGATGACAGTGTGTTGATTAACAAATTAAG 4079
QY 4080 TTGCTCAAG 4139
Db 4080 TTGCTCAAG 4139
QY 4140 TTTATGAG 4199
Db 4140 TTTATGAG 4199
QY 4200 GGAATTAATTAACCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4259
Db 4200 GGAATTAATTAACCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4259
QY 4260 TTTGTTTACCACTTCAATCAATTAATTAATTAATTAATTAATTAATTAATTAAT 4319
Db 4260 TTTGTTTACCACTTCAATCAATTAATTAATTAATTAATTAATTAATTAATTAAT 4319
QY 4320 ACTCAAG 4379
Db 4320 ACTCAAG 4379
QY 4380 TTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4439
Db 4380 TTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4439
QY 4440 ACTTGAAG 4499
Db 4440 ACTTGAAG 4499
QY 4500 AATTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4559
Db 4500 AATTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4559
QY 4560 TATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4619
Db 4560 TATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4619
QY 4620 GCATGACACACAG 4679
Db 4620 GCATGACACACAG 4679
QY 4680 ATGGAAG 4739
Db 4680 ATGGAAG 4739
QY 4740 GAGGAG 4799
Db 4740 GAGGAG 4799
QY 4800 CTTTGTGCTGAG 4859

Db	1321	ACCTGAGCTCACTGCAACCTTCGCTCCAGGTTCAAGCAATTCTCCTGCTCAAGCTTC	1380
Qy	1381	CGGCTAGCTGGAGTACAGGCGGACCGCGGCTAATTTTGTATTTGTAGTAGAGTGG	1440
Db	1381	CGGCTAGCTGGAGTACAGGCGGACCGCGGCTAATTTTGTATTTGTAGTAGAGTGG	1440
Qy	1441	GTTTCACCATATTAAGCCCGGCTGCTTGAACCTCTGACCTGAGTATCCACCACTTC	1500
Db	1441	GTTTCACCATATTAAGCCCGGCTGCTTGAACCTCTGACCTGAGTATCCACCACTTC	1500
Qy	1501	AGCCTCCTAAGTGTGGGATTAAGGCAATGATCAACCGGCGCCGCGCAAGGCTCAGTGT	1560
Db	1501	AGCCTCCTAAGTGTGGGATTAAGGCAATGATCAACCGGCGCCGCGCAAGGCTCAGTGT	1560
Qy	1561	TTAATAAGAAATAACTTGAATGGTTTACTTAACCAACAGGAAACAGACAAAAGCTGTGA	1620
Db	1561	TTAATAAGAAATAACTTGAATGGTTTACTTAACCAACAGGAAACAGACAAAAGCTGTGA	1620
Qy	1621	TAATTTAGGGATTTCTTGGGATGGGGAAATGTGTCCATGAGTGTGCTTACTTCCGAGAC	1680
Db	1621	TAATTTAGGGATTTCTTGGGATGGGGAAATGTGTCCATGAGTGTGCTTACTTCCGAGAC	1680
Qy	1681	CACGTGCTCATCACTTCTTCTCCATCTCATTTTCAAGGCTAGTATACATTTTAT	1740
Db	1681	CACGTGCTCATCACTTCTTCTCCATCTCATTTTCAAGGCTAGTATACATTTTAT	1740
Qy	1741	CACCATGCTTTTGTGGTAAAGCTTCACATGCTTACTGAATAAGATATACATACTAG	1800
Db	1741	CACCATGCTTTTGTGGTAAAGCTTCACATGCTTACTGAATAAGATATACATACTAG	1800
Qy	1801	TTTCATTTGGGGCCATCTGTGTGTGTATAGGGGAGAGGGCATACCCCAAGACTCCT	1860
Db	1801	TTTCATTTGGGGCCATCTGTGTGTGTATAGGGGAGAGGGCATACCCCAAGACTCCT	1860
Qy	1861	TGAAGCCCCCGGAGAGGTTCTCTCAGCTGGGGAGAGCCCTGCAAGCAACCCGAGGTC	1920
Db	1861	TGAAGCCCCCGGAGAGGTTCTCTCAGCTGGGGAGAGCCCTGCAAGCAACCCGAGGTC	1920
Qy	1921	TGGGTGCTGAGGAACCTGCGCAACCCGCGGCACTGGTTGTTTGTATCACTCTCTAG	1980
Db	1921	TGGGTGCTGAGGAACCTGCGCAACCCGCGGCACTGGTTGTTTGTATCACTCTCTAG	1980
Qy	1981	GACCTGTGCTTCTATTTCTGTGTGCTGCTCATTTCAAGGCTATTCAGTATTC	2040
Db	1981	GACCTGTGCTTCTATTTCTGTGTGCTGCTCATTTCAAGGCTATTCAGTATTC	2040
Qy	2041	TATTTAGTACTTATATCTGCAAGACACCAAGACAAATGTGTAGCAAGGCTACCTGC	2100
Db	2041	TATTTAGTACTTATATCTGCAAGACACCAAGACAAATGTGTAGCAAGGCTACCTGC	2100
Qy	2101	CCTACCTTGTGAGGAGTCAAGTTCTCATGAAAGAGTGCAGAAATAATTAATGCA	2160
Db	2101	CCTACCTTGTGAGGAGTCAAGTTCTCATGAAAGAGTGCAGAAATAATTAATGCA	2160
Qy	2161	GCCAACTTAAACCAAGTCTGAAGAAAGAAATAAACACATCTGAAAGAAATGTGCGC	2220
Db	2161	GCCAACTTAAACCAAGTCTGAAGAAAGAAATAAACACATCTGAAAGAAATGTGCGC	2220
Qy	2221	AGCATCCCTTAAACAAAGGCACTCCCTAGAGGCGCCCTGCTGCTCATGATGTCGGAAG	2280
Db	2221	AGCATCCCTTAAACAAAGGCACTCCCTAGAGGCGCCCTGCTGCTCATGATGTCGGAAG	2280
Qy	2281	CCCCCAAGCCGAGCTCTTCCAGGCTCTCTCCATCAGTCAAGGCTGCACTGGCT	2340
Db	2281	CCCCCAAGCCGAGCTCTTCCAGGCTCTCTCCATCAGTCAAGGCTGCACTGGCT	2340
Qy	2341	GCTTCGCTTCCCGTGAATGCTCTGTGTGATCTGAAGTGAAGCTCTTGGCTCCAGGCT	2400
Db	2341	GCTTCGCTTCCCGTGAATGCTCTGTGTGATCTGAAGTGAAGCTCTTGGCTCCAGGCT	2400
Qy	2401	CCAGAAAGAAATGAGAGGAAACTAGTCAACGAGATCTGAGAGGAGACAGTGTTC	2460
Db	2401	CCAGAAAGAAATGAGAGGAAACTAGTCAACGAGATCTGAGAGGAGACAGTGTTC	2460

Qy	2461	CTCAGAGGAAAGGGGCTTCAAGTCTCAGAGAAATTCAGAGGTTGGGACTGCAAGGAG	2520
Db	2461	CTCAGAGGAAAGGGGCTTCAAGTCTCAGAGAAATTCAGAGGTTGGGACTGCAAGGAG	2520
Qy	2521	TGGGAGAGCTGGGCTGAGCGGCTGTGAAGGCGAGAAAGTGAAGGAGGCAAGGCTGA	2580
Db	2521	TGGGAGAGCTGGGCTGAGCGGCTGTGAAGGCGAGAAAGTGAAGGAGGCAAGGCTGA	2580
Qy	2581	GCTGCCAGATGTTCAAGTGTGTTCAAGGCGGCTGGGAGTTTCGCTTCTCTGTAGC	2640
Db	2581	GCTGCCAGATGTTCAAGTGTGTTCAAGGCGGCTGGGAGTTTCGCTTCTCTGTAGC	2640
Qy	2641	CTTTTATCTTTTCTGCTTGGAGGAGAAAGTCTATTTATGTAAGGATGCACTTTC	2700
Db	2641	CTTTTATCTTTTCTGCTTGGAGGAGAAAGTCTATTTATGTAAGGATGCACTTTC	2700
Qy	2701	ATTAAGTCAAGCTGTTAAATTCAGAGGTTGATGAGGTTTCTTCAAGAGGCTTTAT	2760
Db	2701	ATTAAGTCAAGCTGTTAAATTCAGAGGTTGATGAGGTTTCTTCAAGAGGCTTTAT	2760
Qy	2761	TTAATGGGAATATAGAGAGGACTCATTTCTAGGCGGTATTAATTCAGGAAAGTAC	2820
Db	2761	TTAATGGGAATATAGAGAGGACTCATTTCTAGGCGGTATTAATTCAGGAAAGTAC	2820
Qy	2821	TGAGAGTCTTCTTCAATGCTTCTGGGCAACTCAAGCCGCTGTGTGACTTGGCTTA	2880
Db	2821	TGAGAGTCTTCTTCAATGCTTCTGGGCAACTCAAGCCGCTGTGTGACTTGGCTTA	2880
Qy	2881	TGCAAGAGCTGCAAAACCTTGGATCAGAGACTGATTTTCTTCTGTTCTGCAAT	2940
Db	2881	TGCAAGAGCTGCAAAACCTTGGATCAGAGACTGATTTTCTTCTGTTCTGCAAT	2940
Qy	2941	GATTGGTGTGCAACCTGCGGCAAGTGTCTTCTTCTTCTGGGCAATGCTTCTGCT	3000
Db	2941	GATTGGTGTGCAACCTGCGGCAAGTGTCTTCTTCTTCTGGGCAATGCTTCTGCT	3000
Qy	3001	ATTAAGACCTTCAAGCTCTGCTGTCTGTGAACCTTCCGTGATTTCTGTAGGGG	3060
Db	3001	ATTAAGACCTTCAAGCTCTGCTGTCTGTGAACCTTCCGTGATTTCTGTAGGGG	3060
Qy	3061	GATGTTGAGAGGGGAAAGAGGCAAGCTGTGAGCACTGAGCAACAGGAGAGTGAAGG	3120
Db	3061	GATGTTGAGAGGGGAAAGAGGCAAGCTGTGAGCACTGAGCAACAGGAGAGTGAAGG	3120
Qy	3121	GAGACGAGAGGCAAGGAGGCTGGGTGCTCATCAGTCACTGATCAGTCAAGCTC	3180
Db	3121	GAGACGAGAGGCAAGGAGGCTGGGTGCTCATCAGTCACTGATCAGTCAAGCTC	3180
Qy	3181	CAGGACGAGAGCACAATGCTTCAAGAAAGCTCAATGAACCAACAGCAATTTCT	3240
Db	3181	CAGGACGAGAGCACAATGCTTCAAGAAAGCTCAATGAACCAACAGCAATTTCT	3240
Qy	3241	TCCTTAAGCATTAACATGAGCATTTGCCAATAACCAAAAGATGAGAGATTAAGTGT	3300
Db	3241	TCCTTAAGCATTAACATGAGCATTTGCCAATAACCAAAAGATGAGAGATTAAGTGT	3300
Qy	3301	GATAGCTTTTGCCTGAGCTTCAAAAACCTGGGCGAGCAAGTGAATAATGCGAGATTTG	3360
Db	3301	GATAGCTTTTGCCTGAGCTTCAAAAACCTGGGCGAGCAAGTGAATAATGCGAGATTTG	3360
Qy	3361	TTAAAGCTTTTCAACCTGACAGCAACCCACGAGCTCAGAGTGAAGTGTGACAGACGG	3420
Db	3361	TTAAAGCTTTTCAACCTGACAGCAACCCACGAGCTCAGAGTGAAGTGTGACAGACGG	3420
Qy	3421	AGTACCTGCAAGGCGAGGAGGAGAGAAAGAAAGAGAGGATAGTGTATGACCAAGAAAG	3480
Db	3421	AGTACCTGCAAGGCGAGGAGGAGAGAAAGAAAGAGAGGATAGTGTATGACCAAGAAAG	3480
Qy	3481	ACAGATTCATTCAAGGAGGAGTGAATGACCAACAGGATTAATGATCCAGTATCTGG	3540
Db	3481	ACAGATTCATTCAAGGAGGAGTGAATGACCAACAGGATTAATGATCCAGTATCTGG	3540

2221 AGCATCCCTTAACAAGGSCACCTCCCTAGGCCCCCTGCTGCCTCCATCGTSCCGGAG 2280
Db AGCATCCCTTAACAAGGSCACCTCCCTAGGCCCCCTGCTGCCTCCATCGTSCCGGAG 7010
QY 2281 CCCCCAAGCCCGAGTCTTCCAGACCTCTCTCCATCAGTCAAGCGCTGACGTGACCT 2340
Db CCCCCAAGCCCGAGTCTTCCAGACCTCTCTCCATCAGTCAAGCGCTGACGTGACCT 7070
QY 2341 GCTCCGCTTCCCGTGAATCGTCTGTGTGATCTGAGCTGGAACTCTTGGTCCAGGCT 2400
Db GCTCCGCTTCCCGTGAATCGTCTGTGTGATCTGAGCTGGAACTCTTGGTCCAGGCT 7130
QY 2401 CCAGAAAGAAATGAGAGGGAATAGTCTAAACGAGATCTGAGGGGACAGTGTTC 2460
Db CCAGAAAGAAATGAGAGGGAATAGTCTAAACGAGATCTGAGGGGACAGTGTTC 7190
QY 2461 CTCAAGAGGAAAGAGGCGCTTCAAGTCCAGAGAAATTCAGAGGTGGGACCTGCAGGAG 2520
Db CTCAAGAGGAAAGAGGCGCTTCAAGTCCAGAGAAATTCAGAGGTGGGACCTGCAGGAG 7250
QY 2521 TGGGGAAGCTGAGGAGGAGGAGTCTGAAAGGAGGAAAGGAGGAGGAGGAGGAG 2580
Db TGGGGAAGCTGAGGAGGAGGAGTCTGAAAGGAGGAAAGGAGGAGGAGGAGGAG 7310
QY 2581 GCTGCCAGATGTTCAAGTGTGTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
Db GCTGCCAGATGTTCAAGTGTGTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7370
QY 2641 CTTTATCTCTTCTCTGCTGAGAGGAAAGGATCTATTCATGAAAGGAGGAGGAGGAG 2700
Db CTTTATCTCTTCTCTGCTGAGAGGAAAGGATCTATTCATGAAAGGAGGAGGAGGAG 7371
QY 2701 ATAAAGTCACTGTAAATATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2760
Db ATAAAGTCACTGTAAATATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7431
QY 2761 TTAATGGGAATATAGAGAACGAGCTCATTTCTAGGCGGTATATTCAGAGGAGGAGGAG 2820
Db TTAATGGGAATATAGAGAACGAGCTCATTTCTAGGCGGTATATTCAGAGGAGGAGGAG 7491
QY 2821 TGGAGTCTTCTCTTCTGATCTCTGAGCACTGAGCCCTGAGTGTGAGCTTGA 2880
Db TGGAGTCTTCTCTTCTGATCTCTGAGCACTGAGCCCTGAGTGTGAGCTTGA 7551
QY 2881 TGCAGACGAGTCAAAACCTTGGAATCAGAGAGCTCGGTTTCTTCTGCTTGCAT 2940
Db TGCAGACGAGTCAAAACCTTGGAATCAGAGAGCTCGGTTTCTTCTGCTTGCAT 7611
QY 2941 GGTGGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3000
Db GGTGGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7671
QY 3001 ATAAAGACCTTTCAGCTCTGAGTCTCTGTGAACAATTCCCTGTGATCTCTGTGAGGAG 3060
Db ATAAAGACCTTTCAGCTCTGAGTCTCTGTGAACAATTCCCTGTGATCTCTGTGAGGAG 7731
QY 3061 GGAATGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3120
Db GGAATGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7791
QY 3121 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3180
Db GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7851
QY 3181 CAGGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3240
Db CAGGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7911
QY 3241 TCCCTAAGCATAGACATGAGCTTTGCAATATACCAAAAGAAATGAGAGGAGTACGT 3300
Db TCCCTAAGCATAGACATGAGCTTTGCAATATACCAAAAGAAATGAGAGGAGTACGT 7971

3301 GGTAGCTTTGCTGAGCATTTCAAAACCTGGGACAGAGCAAGTGGAAAAATGACAGAGATTG 3360
Db GGTAGCTTTGCTGAGCATTTCAAAACCTGGGACAGAGCAAGTGGAAAAATGACAGAGATTG 8031
QY 3361 TTAACCTTTTCAACCTGACAGACACCCACAGAGTACAGAGTACCTGACAGACAG 3420
Db TTAACCTTTTCAACCTGACAGACACCCACAGAGTACAGAGTACCTGACAGACAG 8091
QY 3421 AGTACCTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3480
Db AGTACCTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8151
QY 3481 ACAGATTCATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3540
Db ACAGATTCATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8211
QY 3541 GTTCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3600
Db GTTCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8271
QY 3601 CCTGATTCATTAATCTATATTTTCTTACAGCTGAGTAACTGAGCAAGTCAAG 3660
Db CCTGATTCATTAATCTATATTTTCTTACAGCTGAGTAACTGAGCAAGTCAAG 8331
QY 3661 GTAGTACTGAGGCTGTAAGATTAAGTTCCTTATTAAGGAGGAGGAGGAGGAGGAG 3720
Db GTAGTACTGAGGCTGTAAGATTAAGTTCCTTATTAAGGAGGAGGAGGAGGAGGAG 8391
QY 3721 GGAATTAAGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3780
Db GGAATTAAGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8451
QY 3781 TAAAGCCAAACAGATTCAGGCTAGGCTTGTGCTGATATATGATGTGTTTGA 3840
Db TAAAGCCAAACAGATTCAGGCTAGGCTTGTGCTGATATATGATGTGTTTGA 8511
QY 3841 CATTCAGGATGTTTATCTATCTGATTCAGAAATAGAGCTAGTACCTTGTGCTG 3900
Db CATTCAGGATGTTTATCTATCTGATTCAGAAATAGAGCTAGTACCTTGTGCTG 8571
QY 3901 TAAACAAACCCAGTTGTAATGTTCAAGTTCAGGCTTAACTGAGAAACCAATCAA 3959
Db TAAACAAACCCAGTTGTAATGTTCAAGTTCAGGCTTAACTGAGAAACCAATCAA 8631
QY 3959 AAGATTAAGATTTTAAAGCAACCTGTGTTTCTCAATCTGAGAGTGTGCTGCAAG 4019
Db AAGATTAAGATTTTAAAGCAACCTGTGTTTCTCAATCTGAGAGTGTGCTGCAAG 8691
QY 4019 CAGTTGGAATATTTACTTCAAGATTAAGACCTGTGTTGTTATTAACAATTAAG 4079
Db CAGTTGGAATATTTACTTCAAGATTAAGACCTGTGTTGTTATTAACAATTAAG 8750
QY 4079 TGCCTAAGGCAATCATTTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4139
Db TGCCTAAGGCAATCATTTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8810
QY 4139 TTTATGAGTATGCAATTTGCTTTTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 4199
Db TTTATGAGTATGCAATTTGCTTTTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 8870
QY 4199 GGAATTTAATTAACCTAAGTCCAGAAAGCTGTGAATTTGAGGAGGAGGAGGAGGAG 4259
Db GGAATTTAATTAACCTAAGTCCAGAAAGCTGTGAATTTGAGGAGGAGGAGGAGGAG 8930
QY 4259 TTTGTTTAAACCACTTCTAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 4319
Db TTTGTTTAAACCACTTCTAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 9049
QY 4319 ACTCAAGTGTGATTAACAGATGCTGTGATTTGCTTACCAATAGAAATCAGACAT 4379
Db ACTCAAGTGTGATTAACAGATGCTGTGATTTGCTTACCAATAGAAATCAGACAT 9050
QY 4379 TTTATCTATATTAACAGTGTGAGATGCTGTGATTTGCTTACCAATAGAAATCAGACAT 4439
Db TTTATCTATATTAACAGTGTGAGATGCTGTGATTTGCTTACCAATAGAAATCAGACAT

QY	84	GGGACCCCTGAGCATTTGCGCTTTAGAGGCGACATTTTAAAGAACTCTTAAGAACTC	900
Dp	841	GGGACCCCTGAGCATTTGCGCTTTAGAGGCGACATTTTAAAGAACTCTTAAGAACTC	900
QY	901	TTGAAAGATCATGAATTTTAAACATTTTAAAGTATTAACAATAATGCGATGCAATATGAG	960
Dp	901	TTGAAAGATCATGAATTTTAAACATTTTAAAGTATTAACAATAATGCGATGCAATATGAG	960
QY	961	TTTAGACATGGGTCCCATTTTATTAAGTCAGGATCAAGGATACGGTGTCCAGCTCC	1020
Dp	961	TTTAGACATGGGTCCCATTTTATTAAGTCAGGATCAAGGATACGGTGTCCAGCTCC	1020
QY	1021	GGATAGGTCAAGAAATCATTAAGAAATCATGTGTGCCATCCTTAACCTTTTTCAGAAATGATC	1080
Dp	1021	GGATAGGTCAAGAAATCATTAAGAAATCATGTGTGCCATCCTTAACCTTTTTCAGAAATGATC	1080
QY	1081	TGTCAATAGCCCTCAACACAGGCGCGAAGTGTCTGACCTTCAACGCAATCTCAACCCCA	1140
Dp	1081	TGTCAATAGCCCTCAACACAGGCGCGAAGTGTCTGACCTTCAACGCAATCTCAACCCCA	1140
QY	1141	GTGCGCTCAACCATTTGTTAACTGTATCATAGTAGTCCCATTAACAATGCGACCTGCC	1200
Dp	1141	GTGCGCTCAACCATTTGTTAACTGTATCATAGTAGTCCCATTAACAATGCGACCTGCC	1200
QY	1201	TGTGACGCCCATCCCGCTTCACAGGAATCTCCCATCTTAAGCTTCGTGATCAAGATGT	1260
Dp	1201	TGTGACGCCCATCCCGCTTCACAGGAATCTCCCATCTTAAGCTTCGTGATCAAGATGT	1260
QY	1261	TACAGCCAAAGCTCCGTGAGGGTATGAGGTGTGTCTTACACTTACCTGATGCTCTAC	1320
Dp	1261	TACAGCCAAAGCTCCGTGAGGGTATGAGGTGTGTCTTACACTTACCTGATGCTCTAC	1320
QY	1321	ACCTGAGCTCATCTGCAACCTTCGCTCCAGGTTCAAGCAATTCCTGTCTGACCTCC	1380
Dp	1321	ACCTGAGCTCATCTGCAACCTTCGCTCCAGGTTCAAGCAATTCCTGTCTGACCTCC	1380
QY	1381	CGCGTAGCTGGGACTACAGGCGACGCCCGGCTAATTTTGTATGTATGTAGAGATGGG	1440
Dp	1381	CGCGTAGCTGGGACTACAGGCGACGCCCGGCTAATTTTGTATGTATGTAGAGATGGG	1440
QY	1441	GTTCACCATATTAGCCCGGCTGTGTAACTCTGACTCAGGTGATCCACCACTCC	1500
Dp	1441	GTTCACCATATTAGCCCGGCTGTGTAACTCTGACTCAGGTGATCCACCACTCC	1500
QY	1501	AGCCTCTTAAGTGTGTGGGATTTACAGGCAATGAGTCAACGCGCCCGGCAAGGGTCAAGT	1560
Dp	1501	AGCCTCTTAAGTGTGTGGGATTTACAGGCAATGAGTCAACGCGCCCGGCAAGGGTCAAGT	1560
QY	1561	TTAATTAAGGAATTAAGTGAATGTGTTACTAAACCAAGAGGAACAGACAAATGCTGTGA	1620
Dp	1561	TTAATTAAGGAATTAAGTGAATGTGTTACTAAACCAAGAGGAACAGACAAATGCTGTGA	1620
QY	1621	TAAATTCAGAGGATTCCTTGAGATGGGGAATGGTGCAAGACTGCGCGCTATGCTCCAGAC	1680
Dp	1621	TAAATTCAGAGGATTCCTTGAGATGGGGAATGGTGCAAGACTGCGCGCTATGCTCCAGAC	1680
QY	1681	CACGTGTCTCATCACTTTCTTCCTCATTCCTCATTTTCAGGCTAAGTTACCAATTTAT	1740
Dp	1681	CACGTGTCTCATCACTTTCTTCCTCATTCCTCATTTTCAGGCTAAGTTACCAATTTAT	1740
QY	1741	CACAGATCTTTGTGTGAAGCTTCACATCTGTATGAAATTAAGATATACATTAACATG	1800
Dp	1741	CACAGATCTTTGTGTGAAGCTTCACATCTGTATGAAATTAAGATATACATTAACATG	1800
QY	1801	TTTCATTTGGGCGCATCTGTGTGTGTATAGGGAGAGGGCATCCCAAGACTCCT	1860
Dp	1801	TTTCATTTGGGCGCATCTGTGTGTGTATAGGGAGAGGGCATCCCAAGACTCCT	1860
QY	1861	TGAAGCCCGGCAAGGTTTCTCTCCAGCTGGGGAGCCTCTGCAAGCACTCCGGGATCC	1920
Dp	1861	TGAAGCCCGGCAAGGTTTCTCTCCAGCTGGGGAGCCTCTGCAAGCACTCCGGGATCC	1920

QY	192	TGGGGTCTCAGACACCTGGCACCCGCGCACATGAGTTGGTTGGTTGTTACCTCTCTAGG	1980
Db	1921	TGGGTGTCTGAGCAACCTGCGACCCGCGCACATGAGTTGGTTGGTTGTTACCTCTCTAGG	1980
QY	1981	GACCTGTGCTTCTATTCTGTGTGACTGTTCATTTCATCCAGGCATTCATTGACAAATT	2040
Db	1981	GACCTGTGCTTCTATTCTGTGTGACTGTTCATTTCATCCAGGCATTCATTGACAAATT	2040
QY	2041	TATTTAGTAACTTATATCTGCGCAGACACACAGAGCAAAATGAGTACAAAGCAGTCACTGC	2100
Db	2041	TATTTAGTAACTTATATCTGCGCAGACACACAGAGCAAAATGAGTACAAAGCAGTCACTGC	2100
QY	2101	CCTACCTCTGTGAGAGTGACAGTTTCTCATGAGAGCGTGCAGAGAAATTTAATAGCA	2160
Db	2101	CCTACCTCTGTGAGAGTGACAGTTTCTCATGAGAGCGTGCAGAGAAATTTAATAGCA	2160
QY	2161	GCCAACTTAAACCCAGTCTGAAAGAAAGAAATTAACCACTTTTGAAGAAATGTGTGC	2220
Db	2161	GCCAACTTAAACCCAGTCTGAAAGAAAGAAATTAACCACTTTTGAAGAAATGTGTGC	2220
QY	2221	AGCATTCCTTAAACAAGGCACCTCCTAGGGCCCCGTGCTCATCTCATGCGCCGAGG	2280
Db	2221	AGCATTCCTTAAACAAGGCACCTCCTAGGGCCCCGTGCTCATCTCATGCGCCGAGG	2280
QY	2281	CCCCCAAGCCGAGTCTTCCAGCTCTCTCTTCATCACTCACAGCTGCAGCTGAGCT	2340
Db	2281	CCCCCAAGCCGAGTCTTCCAGCTCTCTCTTCATCACTCACAGCTGCAGCTGAGCT	2340
QY	2341	GCTCGCTTCCCGTAATCGTCCCTGGGAGCATCGAGCTGAGACATCCTTGGCTCCAGCT	2400
Db	2341	GCTCGCTTCCCGTAATCGTCCCTGGGAGCATCGAGCTGAGACATCCTTGGCTCCAGCT	2400
QY	2401	CCAGAAAGAAATGAGAGGAGAAATAGTCTAAACGAGAACTGAGAGGGGACAGTGTTC	2460
Db	2401	CCAGAAAGAAATGAGAGGAGAAATAGTCTAAACGAGAACTGAGAGGGGACAGTGTTC	2460
QY	2461	CTCAGAGGAAAGGGGCTCCACGTCACAGAAATTCACAGAGTGGGAGATCCAGAGGAG	2520
Db	2461	CTCAGAGGAAAGGGGCTCCACGTCACAGAGAAATTCACAGAGTGGGAGATCCAGAGGAG	2520
QY	2521	TGGGAGACCTGAGGCTGAGCGGAGTGAAGACAGAGAGTGAAGAAAGGCGAAGCTGAA	2580
Db	2521	TGGGAGACCTGAGGCTGAGCGGAGTGAAGAGCGAGAGTGAAGAAAGGCGAAGCTGAA	2580
QY	2581	GCTGCCAGATGTCAGTGTGTTCACGCGGAGGAGTTTCCGTTCCGTGTGAGC	2640
Db	2581	GCTGCCAGATGTCAGTGTGTTCACGCGGAGGAGTTTCCGTTCCGTGTGAGC	2640
QY	2641	CTTTTATCTTTCTCGCTTGGAGAGAAAGTATATTATGAAGATGACATTC	2700
Db	2641	CTTTTATCTTTCTCGCTTGGAGAGAAAGTATATTATGAAGATGACATTC	2700
QY	2701	ATPAAAGTCAGCTGTTAAATTCAGGGTGTGACTGGGTTTCTTCACGAAAGCCTTTAT	2760
Db	2701	ATPAAAGTCAGCTGTTAAATTCAGGGTGTGACTGGGTTTCTTCACGAAAGCCTTTAT	2760
QY	2761	TTAAAGGGAATATGGAAGAGAGTCACTTCCAGGCGGTTAATTCACAGAGAAAGTAC	2820
Db	2761	TTAAAGGGAATATGGAAGAGAGTCACTTCCAGGCGGTTAATTCACAGAGAAAGTAC	2820
QY	2821	TGAGTCTTTCTTCAATGCTTGTGGAGACATCAACCTGTGTGAGACTTGCGTTA	2880
Db	2821	TGAGTCTTTCTTCAATGCTTGTGGAGACATCAACCTGTGTGAGACTTGCGTTA	2880
QY	2881	TGCAGACGCTGAAAACCTTGGAAATCAGAGACTGTGTTTCTTCTGTGTGTGCAATT	2940
Db	2881	TGCAGACGCTGAAAACCTTGGAAATCAGAGACTGTGTTTCTTCTGTGTGTGCAATT	2940
QY	2941	GGTGTGCTGTCAACCGTGGCAAGTGTCTCTCTTCCCTGGGCAATAGTCTTCTGCT	3000
Db	2941	GGTGTGCTGTCAACCGTGGCAAGTGTCTCTCTTCCCTGGGCAATAGTCTTCTGCT	3000
QY	3001	ATPAAAGCCTTGCAGCTCTGTGTTCTGTGAACATTCCTGTGATTTCTGTGAGGGG	3060

Db	3001	ATAAAGACCCCTTGCAGCTCTGTGTCTGTGAACACTTCCCTGTGATTTCTCTGTGAAGGG	3060
Qy	3061	GGATGTTGAGGGGGAAGAGGACAGAGCTGAGCAGCTGAAGCCACAGGGAGGTGAGGG	3120
Db	3061	GGATGTTGAGGGGGAAGAGGACAGAGCTGAGCAGCTGAAGCCACAGGGAGGTGAGGG	3120
Qy	3121	GGACAGGAGGACAGGACGAGAGCTGGGTCTCACTAGCCCACTGATPACAGTGAAGCTC	3180
Db	3121	GGACAGGAGGACAGGACGAGAGCTGGGTCTCACTAGCTCTCACTGATPACAGTGAAGCTC	3180
Qy	3181	CAGGACCGAGAGCCACATGTCTTGAGAAAGCTCAATGAACCCAAACAGCCACATTTTCT	3240
Db	3181	CAGGACCGAGAGCCACATGTCTTGAGAAAGCTCAATGAACCCAAACAGCCACATTTTCT	3240
Qy	3241	TCCTTAAGCATATGACATGCGATTTGCGCAATACCAAAAAGATGCGAGACTATCTGT	3300
Db	3241	TCCTTAAGCATATGACATGCGATTTGCGCAATACCAAAAAGAGCGAGACTATCTGT	3300
Qy	3301	GGTAGCTTTTCCCTGCGCATTTCAAAAACCTGGGCCAGAGCAGTGTGAATATGCGAGATTG	3360
Db	3301	GGTAGCTTTTCCCTGCGCATTTCAAAAACCTGGGCCAGAGCAGTGTGAATATGCGAGATTG	3360
Qy	3361	TTAAACCTTTTCACCCTGACGAGCAACCCACGAGCTGACAGTAGCTGTGACAGCAGG	3420
Db	3361	TTAAACCTTTTCACCCTGACGAGCAACCCACGAGCTGACAGTAGCTGTGACAGCAGG	3420
Qy	3421	AGTACCTGCGACGCGCAGGGGAGGAGAAAGAAAGAGGATATGTATATGACAGAAAG	3480
Db	3421	AGTACCTGCGACGCGCAGGGGAGGAGAAAGAAAGAGGATATGTATATGACAGAAAG	3480
Qy	3481	ACAGATTCATTTCAAGGCGAGTGGGATTTGACACAGGATTTATATGCTCACGCTATCTCG	3540
Db	3481	ACAGATTCATTTCAAGGCGAGTGGGATTTGACACAGGATTTATATGCTCACGCTATCTCG	3540
Qy	3541	GTTCTAGAGGCGAGGCTATATTTGTGGGGGAAAAAATCACTTCAAGGAAAGTGGAGAG	3600
Db	3541	GTTCTAGAGGCGAGGCTATATTTGTGGGGGAAAAAATCACTTCAAGGAAAGTGGAGAG	3600
Qy	3601	CCTGATTTCTATACTATATTTTCTTTCCTTACAGCTGAGTATTTCTGAGCAAGTCAAG	3660
Db	3601	CCTGATTTCTATACTATATTTTCTTTCCTTACAGCTGAGTATTTCTGAGCAAGTCAAG	3660
Qy	3661	GTAAGTACTGAGGCTGTAGATTACTTAAGTTCTTCTTATTAAGAACTCTTTTCTCTGT	3720
Db	3661	GTAAGTACTGAGGCTGTAGATTACTTAAGTTCTTCTTATTAAGAACTCTTTTCTCTGT	3720
Qy	3721	GGAGTTACACACACAGGGGCAATCCCGTTCTTTTACAGGAAGAAACATTCCTTAAG	3780
Db	3721	GGAGTTACACACACAGGGGCAATCCCGTTCTTTTACAGGAAGAAACATTCCTTAAG	3780
Qy	3781	TAAAGCCAAACAGATTCAAGCCTAGGCTTGCTGACTATATGATGTGTTTTTGAATAAT	3840
Db	3781	TAAAGCCAAACAGATTCAAGCCTAGGCTTGCTGACTATATGATGTGTTTTTGAATAAT	3840
Qy	3841	CATTTCAGCGATGTTTACTATCTGATTTAGAAATGAGACTAGTAACTTCCTTGGTCACTG	3900
Db	3841	CATTTCAGCGATGTTTACTATCTGATTTAGAAATGAGACTAGTAACTTCCTTGGTCACTG	3900
Qy	3901	TAAACAAACACCCAGTTGTAATATGCTCAAGTTCAAGGTTTAATGCGAAGCAATCAAA	3959
Db	3901	TAAACAAACACCCAGTTGTAATATGCTCAAGTTCAAGGTTTAATGCGAAGCAATCAAA	3959
Qy	3961	AAGATATGAATCTTTAGCAAACTGTGTCTTCCAC-TCTGAGAGTGAAGTCTCCACGG	4019
Db	3961	AAGATATGAATCTTTAGCAAACTGTGTCTTCCAC-TCTGAGAGTGAAGTCTCCACGG	4019
Qy	4020	CAGTTTGAATAATTTACTTCAACAGTATGCACTGTGTTGGTATTAACAACATAAG	4079
Db	4020	CAGTTTGAATAATTTACTTCAACAGTATGCACTGTGTTGGTATTAACAACATAAG	4079
Qy	4080	TTGCTCAAGGCAATCATTAATTTCAAGTGGCTTAAAGTTACTCTTGACAGTTTGGTATA	4139

D	4080	TTGGCTCAAGGCAATCATTTATTTCAAGTGGCTTAAGTTACTTGCAGATTTGGTATA	4139
Q	4140	TTTATTTGGCTATTTGGCAATTTGGCTTTTGTCTTTTCTCTTTGGGCTTATTAATGTAAGCA	4139
D	4140	TTTATTTGGCTATTTGGCAATTTGGCTTTTGTCTTTTCTCTTTGGGCTTATTAATGTAAGCA	4139
Q	4200	GGGATTTATTAACCTACAGTCACAGAACCGTGAAATTTGATGAGGAAAAATTACATTT	4259
D	4200	GGGATTTATTAACCTACAGTCACAGAACCGTGAAATTTGATGAGGAAAAATTACATTT	4259
Q	4260	TTGTTTTTACCACTTCTTAACTAAATTTAACATTTTATTCATTGGCAATAGAGCATTA	4319
D	4260	TTTATTTTACCACTTCTTAACTAAATTTAACATTTTATTCATTGGCAATAGAGCATTA	4319
Q	4320	ACTCAAGTGGTAAATAACAGTACGTGGATTTTGTATATACAAATAGAAATCAAGACAT	4379
D	4320	ACTCAAGTGGTAAATAACAGTACGTGGATTTTGTATATACAAATAGAAATCAAGACAT	4379
Q	4380	TTTATACTAATAATACAGTTGTTCAGAAAGTTGTAAGTGAATAATTTATCTCAAACT	4439
D	4380	TTTATACTAATAATACAGTTGTTCAGAAAGTTGTAAGTGAATAATTTATCTCAAACT	4439
Q	4440	ACTTTGAAATTAAGCTCCCTCGCTGGAATCTTGTTTTAAATTTAAATCAATGTTAA	4499
D	4440	ACTTTGAAATTAAGCTCCCTCGCTGGAATCTTGTTTTAAATTTAAATCAATGTTAA	4499
Q	4500	AATTTGATTTTGTATATATATATTTCAATTTATCATTTGTTCCTTGTATATATATTT	4559
D	4500	AATTTGATTTTGTATATATATATTTCAATTTATCATTTGTTCCTTGTATATATATTT	4559
Q	4560	TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCAAGATTTCCACATAGAGTTCTG	4619
D	4560	TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCAAGATTTCCACATAGAGTTCTG	4619
Q	4620	GGATGCACACACACAGAGTAAAGACATGATTTAGAGCTTAACTATACATTTGGTGGCTAG	4679
D	4620	GGATGCACACACACAGAGTAAAGACATGATTTAGAGCTTAACTATACATTTGGTGGCTAG	4679
Q	4680	ATGCAGAAGCTGAAAATTGAAAAGTTCTTCCCAAGATACACAGTTGTTTAAAGTGGGCT	4739
D	4680	ATGCAGAAGCTGAAAATTGAAAAGTTCTTCCCAAGATACACAGTTGTTTAAAGTGGGCT	4739
Q	4740	GAGGGGGGGAATTCGCGGCTTCTATAGGAATGCTCCCTGGAGGCTGGTAGGGTCTGT	4799
D	4740	GAGGGGGGGAATTCGCGGCTTCTATAGGAATGCTCCCTGGAGGCTGGTAGGGTCTGT	4799
Q	4800	CTTGTGTCTGCGCTGCTGTAAATTTTCTCTGTCCCTGCTACGTTTAAAGCACTTGT	4859
D	4800	CTTGTGTCTGCGCTGCTGTAAATTTTCTCTGTCCCTGCTACGTTTAAAGCACTTGT	4859
Q	4860	TGGAATCTCAAGTTCCCTACATAGTGGCTGGACAATGCGAGTTCTCAATGATTTGGACA	4919
D	4860	TGGAATCTCAAGTTCCCTACATAGTGGCTGGACAATGCGAGTTCTCAATGATTTGGACA	4919
Q	4920	GTCATTTGGAATTAACCTAGAAATATCTTGTGGAATACAGACACACACAGTATGCTGT	4979
D	4920	GTCATTTGGAATTAACCTAGAAATATCTTGTGGAATTAACAGACACACACAGTATGCTGT	4979
Q	4980	GTTGTAAGTGTGTGTAAC----GTGTGTGTGTGTGTGTGTGTGTGTGTAATAACAGGTGG	5039
D	4980	GTTGTAAGTGTGTGTAAC----GTGTGTGTGTGTGTGTGTGTGTGTGTAATAACAGGTGG	5039
Q	5036	AATATTAAGAACTTAAATTTGGGGGTAAGGGGATTAATTTGGGATGTTCTTTTAAAGA	5099
D	5040	AATATTAAGAACTTAAATTTGGGGGTAAGGGGATTAATTTGGGATGTTCTTTTAAAGA	5099
Q	5096	AACTCAAAACAGACTTCTGAAAGTTATTTCTTAAGAACTTTGCTGGACAGCGTGAAGCA	5159
D	5100	AACTCAAAACAGACTTCTGAAAGTTATTTCTTAAGAACTTTGCTGGACAGCGTGAAGCA	5159
Q	5156	ACCCCTCGGTGACAGGCCCAACCCAGAGCTACAGTGGCAACCTGTCTCCCTCCCA	5219
D	5160	ACCCCTCGGTGACAGGCCCAACCCAGAGCTACAGTGGCAACCTGTCTCCCTCCCA	5219

